

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 3, 2002, 15:38:38 ; Search time 53.39 seconds

(without alignments)
667.816 Million cell updates/sec

Title: US-09-945-182-26

Perfect score: 1757

Sequence: 1 NSDLSHTPLRRQKYLFDVSM.....GNVVYKQYEDMWVESCGR 321

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_032802.*

- 1: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT.*
- 2: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT.*
- 3: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT.*
- 4: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT.*
- 5: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1984.DAT.*
- 6: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1985.DAT.*
- 7: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1986.DAT.*
- 8: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1987.DAT.*
- 9: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1988.DAT.*
- 10: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1989.DAT.*
- 11: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1990.DAT.*
- 12: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1991.DAT.*
- 13: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1992.DAT.*
- 14: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1993.DAT.*
- 15: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1994.DAT.*
- 16: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1995.DAT.*
- 17: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1996.DAT.*
- 18: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1997.DAT.*
- 19: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT.*
- 20: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT.*
- 21: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.*
- 22: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1757	100.0	321	16	AA198730 Human mature VL-1
2	1757	100.0	321	18	AAW26591 Human bone morphog
3	1757	100.0	321	22	AAE10982 Human full length
4	1747	99.4	455	22	AAW50216 Human growth/diffe
5	1368	77.9	436	17	AAW95636 Cartilage-derived
6	1207.5	68.7	263	16	AAW26591 Murine mV2 protein
7	1207.5	68.7	263	18	AAW26595 Murine BMP-13 homo
8	1202.5	68.4	263	22	AAE10985 Murine partial mV2
9	771	43.9	401	14	AAW40800 TGF-beta-like clon
10	771	43.9	501	16	AAW69600 New TGF-beta fami
11	771	43.9	501	18	AAW36100 Human MP52. Homo

12	771	43.9	501	18	AAW19210 Human TGF-beta pro
13	771	43.9	501	18	AAW11900 Human high mol. wt
14	771	43.9	501	18	AAW01799 Human MP52 protein
15	771	43.9	501	18	AAW12770 Human bone morphog
16	771	43.9	501	19	AAW44868 TGF-beta superfami
17	771	43.9	501	19	AAW33008 Human MP52. Homo
18	765	43.5	388	16	AAW8734 Human bone morphog
19	765	43.5	388	18	AAW26592 Human bone morphog
20	765	43.5	388	22	AAE10986 Human bone morphog
21	765	43.5	495	15	AAE60022 Growth differentia
22	765	43.5	495	22	AAW84550 Amino acid sequenc
23	762	43.4	501	17	AAW95635 Cartilage-derived
24	762	43.4	501	21	AAW92034 Human growth diffe
25	760	43.3	501	22	AAW70529 Human TGF-beta MP5
26	731	41.6	134	16	AAW66867 GDF-6. Mus sp. A
27	731	41.6	134	21	AAW12986 Murine growth diff
28	691.5	39.4	294	16	AAW8739 Human bone morphog
29	691.5	39.4	294	18	AAW26589 Human bone morphog
30	691.5	39.4	294	22	AAE10972 Human bone morphog
31	618	35.2	240	16	AAW8738 Murine mV1 protein
32	618	35.2	240	18	AAW26594 Murine BMP-12 homo
33	618	35.2	240	22	AAE10984 Murine partial mV1
34	601	34.2	184	22	ABG29375 Novel human diagno
35	584	33.2	411	16	AAW8740 Fusion of BMP-2 pr
36	584	33.2	411	18	AAW26597 BMP-2 propeptide/B
37	584	33.2	411	22	AAE10983 Human BMP2 propept
38	575	32.7	102	21	AAW09554 Human CDMP-2/GDF-6
39	575	32.7	102	21	AAW02820 Human CDMP-2/GDF-6
40	575	32.7	102	21	AAW92579 CDMP-2/GDF-6 finge
41	572	32.6	102	21	AAW09555 Mouse GDF-6, SEQ
42	572	32.6	102	21	AAW02821 Mouse GDF-6 amino
43	572	32.6	102	21	AAW92580 GDF-6 finger-1-hee
44	563	32.0	102	21	AAW09556 Bovine CDMP-2, SE
45	563	32.0	102	21	AAW02822 Bovine CDMP-2 amin

ALIGNMENTS

RESULT 1

AAW8730

ID AAR78730 standard; Protein; 321 AA.

XX

AC AAR78730;

XX

DT 30-NOV-1995 (first entry)

DE Human mature VL-1 (BMP-13) encoding sequence.

XX

XX Bone morphogenetic protein; VL-1; tendon; ligament; tendinitis.

XX Homo sapiens.

XX

Key Location/Qualifiers

FT Peptide 1..201

FT Protein 202..321

FT /label= mature protein

FT Misc-difference 202..321

FT /note= "claimed"

FT Misc-difference 220..321

FT /note= "claimed"

XX

PN WO9516035-A.

XX

XX 15-JUN-1995.

XX

XX 06-DEC-1994; 94WO-US14030.

XX

XX 02-NOV-1994; 94US-0333576.

PR 07-DEC-1993; 93US-0164103.

PR 25-MAR-1994; 94US-0217780.

XX

PA (GEM) GENETICS INST INC.

PA (HARD) HARVARD COLLEGE.
 XX Celeste AJ, Melton DA, Rosen VA, Thomsen GH, Wolfman NM;
 PI Wozney JM;
 XX WPI: 1995-224320/29.
 DR N-PSDB; AAQ96208.
 XX Bone morphogenetic proteins -12 and -13 and corresp. DNA - used in
 PT compsn. for inducing tendon/ligament-like tissue formation
 XX Claim 14; Page 62-64; 84pp; English.
 XX BMP-12 related proteins are a subset of the BMP/TGF-beta/Vg-1
 CC family of proteins, including BMP-12 and Vg-1. Vg-1 is designated
 CC BMP-13. Like BMP-12, it is expected that BMP-13, as expressed by
 CC mammalian cells such as CHO cells, exists as a heterogeneous popn.
 CC of active species of BMP-13 protein with varying N-termini. It is
 CC expected that all active species will contain the AA sequence
 CC beginning with the 19th Cys residue of the mature protein until
 CC the 119th residue of the mature protein or until the stop codon
 CC after the 120th residue of the mature protein. Other active
 CC species contain additional AA sequence in the N-terminal direction.
 CC AAQ96208 is a partial DNA sequence and AAR78730 is the derived AA
 CC sequence of a portion of the 2.5 kb DNA insert of the plasmid
 CC subclone pGENJLDC31/2.5, derived from clone lambdaJLDC31.
 XX Sequence 321 AA;
 SQ

Query Match 100.0%; Score 1757; DB 16; Length 321;
 Best Local Similarity 100.0%; Pred. No. 8.2e-149;
 Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NSDSLSTPLRRQKYLFDVSMLSKDEELVGAELRLFRQAPSAPGWPPAGPLHVQLFPCCLSP 60
 Db 1 NSDSLSTPLRRQKYLFDVSMLSKDEELVGAELRLFRQAPSAPGWPPAGPLHVQLFPCCLSP 60

Qy 61 LLLDARTLDPOGAPAGWEVFDVWQGLRHQPWKQLCLELRAAANGELDAGEAEARAGPQ 120
 Db 61 LLLDARTLDPOGAPAGWEVFDVWQGLRHQPWKQLCLELRAAANGELDAGEAEARAGPQ 120

Qy 121 PPPDLRLSLGFRVRPPQERALLVVFTRSQKNLFAEMREQLGSAAAGPAGAGEGSWP 180
 Db 121 PPPDLRLSLGFRVRPPQERALLVVFTRSQKNLFAEMREQLGSAAAGPAGAGEGSWP 180

Qy 181 PPSGAPDARPLSPGRRRRRTAFASRHGKRHGKSKRLRCSKPLHVNFKELGWDWIIA 240
 Db 181 PPSGAPDARPLSPGRRRRRTAFASRHGKRHGKSKRLRCSKPLHVNFKELGWDWIIA 240

241 PLEYEAYHCEGVGCDPLRSHLEPTNHALIOTLNMSPDGGSTPPSCCVPTKITPISILYID 300
 Db 241 PLEYEAYHCEGVGCDPLRSHLEPTNHALIOTLNMSPDGGSTPPSCCVPTKITPISILYID 300

Qy 301 AGNNVYKQYEDVMVESGCR 321
 Db 301 AGNNVYKQYEDVMVESGCR 321

RESULT 2

AAW26591
 ID AAW26591 standard; Protein; 321 AA.

AC AAW26591;

DT 21-JAN-1998 (first entry)

XX Human bone morphogenetic protein BMP-13.

DE BMP-13; bone morphogenetic protein; human; tendon; ligament;
 KW wound healing; tissue repair; tendonitis; carpal tunnel syndrome;
 KW therapy.

XX

OS Homo sapiens.
 XX Key
 FH Peptide 1..201
 FT /label= sig_peptide
 FT Protein 202..321
 FT /label= Mat_protein
 FT /note= "Claim 5"
 FT 218..294
 FT /note= "Claim 5"
 XX US5658882-A.
 XX 19-AUG-1997.
 PD 07-DEC-1993; 93US-0164103.
 XX 22-DEC-1994; 94US-0362670.
 PR 07-DEC-1993; 93US-0164103.
 PR 25-MAR-1994; 94US-0217780.
 PR 02-NOV-1994; 94US-0333576.
 XX (GEMY) GENETICS INST INC.
 PA (HARD) HARVARD COLLEGE.
 XX Celeste AJ, Melton DA, Rosen VA, Thomsen GH, Wolfman NM;
 PI Wozney JM;
 XX WPI: 1997-424270/39.
 DR N-PSDB; AAT90386.
 XX Inducing tendon and ligament formation using BMP-12, BMP-13 or MP-52
 PT - useful for tissue healing and repair, treatment of tendonitis,
 PT improving fixation of tendons to bone etc
 XX Claim 5; Column 57-60; 43pp; English.
 CC This polypeptide comprises a novel bone morphogenetic protein, its
 CC designated BMP-13 that induces tendon and ligament formation. Its
 CC amino acid sequence was deduced from isolated genomic clone vi-1
 CC (see AAT90386). A claimed method for inducing formation of tendon
 CC and/or ligament tissues involves the administration of a
 CC composition containing at least one protein selected from BMP-13,
 CC MP52 (see AAW26590) and BMP-12 (see AAW26589). The method is used for
 CC tissue (including skin) healing and repair. This is useful for
 CC treating tendonitis, carpal tunnel syndrome and other defects of
 CC traumatic or congenital origin, in cosmetic surgery and to improve
 CC fixation of tendons or ligaments to bone. The specified proteins
 CC can also be used to increase activity of other BMPs e.g. BMP-2
 CC (see AAW26597).
 XX Sequence 321 AA;
 SQ

Query Match 100.0%; Score 1757; DB 18; Length 321;
 Best Local Similarity 100.0%; Pred. No. 8.2e-149;
 Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NSDSLSTPLRRQKYLFDVSMLSKDEELVGAELRLFRQAPSAPGWPPAGPLHVQLFPCCLSP 60
 Db 1 NSDSLSTPLRRQKYLFDVSMLSKDEELVGAELRLFRQAPSAPGWPPAGPLHVQLFPCCLSP 60

Qy 61 LLLDARTLDPOGAPAGWEVFDVWQGLRHQPWKQLCLELRAAANGELDAGEAEARAGPQ 120
 Db 61 LLLDARTLDPOGAPAGWEVFDVWQGLRHQPWKQLCLELRAAANGELDAGEAEARAGPQ 120

Qy 121 PPPDLRLSLGFRVRPPQERALLVVFTRSQKNLFAEMREQLGSAAAGPAGAGEGSWP 180
 Db 121 PPPDLRLSLGFRVRPPQERALLVVFTRSQKNLFAEMREQLGSAAAGPAGAGEGSWP 180

Qy 181 PPSGAPDARPLSPGRRRRRTAFASRHGKRHGKSKRLRCSKPLHVNFKELGWDWIIA 240
 Db 181 PPSGAPDARPLSPGRRRRRTAFASRHGKRHGKSKRLRCSKPLHVNFKELGWDWIIA 240

QY 241 PLEYEAYHCEGVCDPLRSHLEPTNHAIIQTLMSMDPGSTPPSCCVPTKLTPIISILYID 300
 |||||
 Db 241 pleyeayhcegvcdplrshleptnhaIIqtlmsmdpgstppscvptkltpisilyid 300
 |||||
 QY 301 AGNNVYKQYEDMVVESCGR 321
 |||||
 Db 301 agnnvykyedmvvescgr 321
 |||||

RESULT 3
 AAE10982
 ID AAE10982 standard; Protein: 321 AA.
 XX
 AC AAE10982;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 XX Human full length VL-1 or BMP-13 protein.
 XX
 XX Human: bone morphogenic protein; BMP-13; vulnerary; antiinflammatory;
 KW analgesic; gene therapy; transforming growth factor-beta; TGF-beta;
 KW tissue formation; wound healing; tissue repair; ligament defect; VL-1;
 XX carpal tunnel syndrome; tendonitis.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..201
 FT /label= Signal_peptide
 FT Protein 202..321
 FT /label= Mature_BMP_12_protein
 FT
 XX
 PN US6284872-B1.
 XX
 XX 04-SEP-2001.
 XX
 XX 28-FEB-1997; 97US-0808324.
 XX
 PR 22-DEC-1994; 94US-0362670.
 PR 07-DEC-1993; 93US-0164103.
 PR 25-MAR-1994; 94US-0217780.
 PR 02-NOV-1994; 94US-0333576.
 XX
 XX (GEMY) GENETICS INST INC.
 PA (HARD) HARVARD COLLEGE.
 XX
 XX Celeste AJ, Wozney JM, Rosen VA, Wolfman NM, Thomsen GH;
 Melton DA;
 DR WPI: 2001-588978/66.
 XX N-PSDB; AAD18333.
 XX
 FT New chimeric DNAs, useful for treating tendonitis, carpal tunnel
 PT syndrome and other tendon and ligament defects, comprises DNA encoding
 PT propeptide linked to DNA encoding bone morphogenetic proteins (BMP)-12,
 PT BMP-13 or MP52 -
 XX
 XX Example 1; Column 57-60; 42pp; English.
 PS
 XX
 XX The invention relates to a chimeric DNA comprising a DNA sequence
 CC encoding a propeptide from a member of the transforming growth factor
 CC (TGF)-beta superfamily of proteins. This DNA is linked to a DNA sequence
 CC encoding an amino acid sequence encoding a mature polypeptide consisting
 CC of Bone Morphogenetic Protein (BMP)-12, BMP-13 or MP52 protein. The DNA
 CC sequences are useful for producing proteins which induce tendon/ligament
 CC like tissue formation, and for isolating and cloning further DNA
 CC sequences encoding BMP-12 related proteins with similar activity. The
 CC proteins are useful for the induction of tendon/ligament-like tissue
 CC formation, wound healing, ligament and other tissue repair, augmenting
 CC the activity of bone morphogenetic proteins, and for treating tendonitis,
 CC carpal tunnel syndrome and other tendon and ligament defects. The
 CC present sequence is human VL-1 protein also designated as BMP-13.

XX Sequence 321 AA;
 SQ
 Query Match 100.0%; Score 1757; DB 22; Length 321;
 Best Local Similarity 100.0%; Pred. No. 8.2e-149;
 Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NSDLSHTPLRQKYLEFDVSMLSKDELVGAEELRLEFRQAPSPAGPAGPLHVQLFPCLSP 60
 |||||
 Db 1 nsdlshtplrqrkylfdvsmldskdelvgaelrfraqpsapwppagplhvqlfclsp 60
 |||||
 QY 61 LLLDARTLDPOGAPPAGWEVDFVWQGLRHQPWKQLCLELRAANGELDAGEAEARARGPQ 120
 |||||
 Db 61 lllidartldpqgappagwevdfwqglrhqpwkqlclelraaageldageaeeararqpq 120
 |||||
 QY 121 PPPPDLRSLGFRVRPPQERALLVFTSRQKNLFAEMREQLGSAEAGPGAGAGSGWP 180
 |||||
 Db 121 ppppdlrslgfrvrppqerallvftsrqknlfamreqlgsaeagpgagagsgwp 180
 |||||
 QY 181 PPSGAPDARPLSPGRRRRRTAFASRHGKRSRLRCSKKPLHVNFKELGWDWIIA 240
 |||||
 Db 181 ppsgapdarplspgrrrrrtafasrhgkrsrlrckskkplhvnfkelnwddwila 240
 |||||
 QY 241 PLEYEAYHCEGVCDPLRSHLEPTNHAIIQTLMSMDPGSTPPSCCVPTKLTPIISILYID 300
 |||||
 Db 241 pleyeayhcegvcdplrshleptnhaIIqtlmsmdpgstppscvptkltpisilyid 300
 |||||

RESULT 4
 AAM50216
 ID AAM50216 standard; Protein: 455 AA.
 XX
 AC AAM50216;
 XX
 DT 07-JAN-2002 (first entry)
 XX
 DE Human growth/differentiation factor-6-like protein AMF10.
 XX
 KW AMF10; human; growth/differentiation factor-6; cancer;
 XX cell proliferation; astrocytoma; glioma; therapy; diagnosis.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..22
 FT /label= Signal_peptide
 FT Protein 23..455
 FT /label= Mature_protein
 FT
 XX WO200174897-A2.
 PN
 XX 11-OCT-2001.
 PD
 XX
 XX 03-APR-2001; 2001WO-US10892.
 PF
 XX
 XX 03-APR-2000; 2000US-194314P.
 PR
 XX 16-AUG-2000; 2000US-225693P.
 XX
 XX (CURA-) CURAGEN CORP.
 PA
 XX Vernet CAM, Burgess CE, Fernandes E, Taupier RJ, Quinn KE;
 PI Spytek KA, Rastelli L, Herrmann JL;
 XX
 XX WPI: 2001-626395/72.
 DR N-PSDB; AAI70203.
 XX
 XX New AMF1-10 polypeptides and encoding polynucleotides, useful for
 PT treating or preventing disorders related to modulation of cell

PT movement, cell signal processing, cell adhesion or migration pathways
PT e.g., cancer
XX
PS Claim 1: Page 44-45: 134pp; English.
XX
CC The present sequence is that of the novel, secreted human
CC growth/differentiation factor-6 (GDF6)-like protein, AMF10.
CC AMF10 is expressed in astrocytoma and glioma-derived tissue. DNA
CC encoding the AMF8 may be useful in gene therapy, and the protein
CC may also be used as a therapeutic, especially in treatment of
CC cancer and other cell proliferative disorders. Generally, the
CC AMF1-10 (AMFX) nucleic acids and proteins of the invention are useful
CC for treating or preventing AMFX-associated disorders, e.g. a disorder
CC related to cell signal processing and metabolic pathway modulation,
CC cell adhesion or migration pathway modulation, chemoresistance,
CC radiotherapy resistance, survival in trophic factor limited
CC secondary tissue site microenvironments, connective tissue
CC disorders, tissue remodeling, oncogenesis, cancer of the breast,
CC ovary, cervix, prostate, endometrium, stomach, colon, lung,
CC bladder, kidney, brain, and soft-tissue, cellular transformation,
CC developmental tissue remodeling, inflammation, blood clot
CC formation and resorption, haematopoiesis, angiogenesis, multidrug
CC resistance related to organic anion transporters, malignant disease
CC progression, autocrine and paracrine regulation of cell growth, and
CC cellular responses to external stimuli, and other diseases,
CC disorders, etc. (all claimed). AMFX proteins are also used for
CC screening drugs or compounds that modulate AMFX protein activity or
CC expression as well as to treat disorders characterized by
CC insufficient or excessive production of AMFX protein.
XX
SQ Sequence 455 AA;

Query Match 99.4%; Score 1747; DB 22: Length 455;
Best Local Similarity 100.0%; Pred. No. 9.8e-148;
Matches 319; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 3 DLSHTPLRRQKYLFDVSMLELSDKEELVGAELRLFRQAPSAPMGPPAGPLHVQLFPCLSPLL 62
Db 137 dlshtplrrqkylfdvsmlelsgaelrlfrqapsapmgppagplhvqlfpcispll 196
Oy 63 LDARTLDPQAGPAGVEVFDVWGLRHQPWKQLCLELRAAWGELDAGEAEARARGPQQPP 122
Db 197 ldartldpqagpagvevfdvwwglrhqpwkqlclelraawgeldageaeatargpqqpp 256
Oy 123 PPDLRSIGFGRVRPPOERALLVVFTRSQKLNLFAMREQLGSAEAGPAGAGEGSWPPP 182
Db 257 ppdlrslgfgrrvrrppqerallvvtfsqrknlfaemreqlgasaeagpgagewswppp 316
183 SGAPDARPLPSPGRRRRRTAFASRHGKRSRLRCSKKPLHVNFKELGWDWIIAPL 242
317 sgapdarplpspgrrrrrtafasrhgkrsrlrcskskplhvnfkclgwdwdwiapl 376
Oy 243 EYAYHCEGVCDFPLRSHLEPTNHAIIQTLMNSMDPGSTPPSCCVPTKLTPIISILYIDAG 302
Db 377 eyeayhcegvcdflrshleptnhaiqltlnmsmdpgstppscvptkltptisilyidag 436
Oy 303 NNVVYKQYEDMVVESCGR 321
Db 437 nnvvykyedmvvvescgr 455
RESULT 5
ID AAR95636 standard; Protein; 436 AA.
XX
AC AAR95636;
DT
XX
DT 25-OCT-1996 (first entry)
XX
DE Cartilage-derived morphogenetic protein-2.
XX
KW Cattle; cartilage-derived morphogenetic protein-2; CDMP-2;

KW articular cartilage; chondrogenic; vulnery; implantation;
KW chondromalacia; osteoarthritis; therapy; joint repair.
XX
OS Bos taurus.
XX
FH Key Location/Qualifiers
FT Region 1..312
FT /note= "pro-region"
FT Modified-site 89..91
FT /note= "N-glycosylation site"
FT Cleavage-site 313..316
FT /note= "proteolytic processing site"
FT Domain 317..436
FT /note= "C-terminal mature domain"
FT Peptide 352..382
FT /note= "Consensus conserved motif (AAR95641)"
XX
PN WO9614335-A1.
XX
XX 17-MAY-1996.
PD
XX 07-NOV-1994; 94WO-US12814.
PF
XX 07-NOV-1994; 94WO-US12814.
PR
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA
XX Chang SC, Luyten FP, Moos M;
PI
XX WPI; 1996-251714/25.
DR N-PSDB; AAT31602.
XX
PT New purified cartilage extracts and proteins - used to stimulate the
PT development and repair of cartilage in vivo.
XX
PS Claim 11; Fig 2; 34pp; English.
XX
CC The sequence represents cattle articular cartilage-derived
CC morphogenetic protein-2 (CDMP-2). The N-terminal methionine and
CC signal peptide is missing, but part of the pro-region, a typical
CC proteolytic cleavage site and a C-terminal domain containing 7
CC highly conserved Cys residues characteristic of the transforming
CC growth factor-beta gene family are present. A single N-glycosylation
CC site is located in the pro-region. A consensus highly conserved
CC motif in CDMP proteins (AAR95641) is present in the C-terminal domain.
CC CDMP-2 is present in a purified cartilage extract (claimed) which
CC stimulates local cartilage formation and repair when combined with a
CC matrix and implanted in a mammal. The protein may be used in therapy
CC of e.g. chondromalacia or osteoarthritis, to heal joint surfaces, or
CC to repair cartilage after reconstructive surgery.
XX
SQ Sequence 436 AA;
Query Match 77.9%; Score 1368; DB 17: Length 436;
Best Local Similarity 81.7%; Pred. No. 6.6e-114;
Matches 268; Conservative 9; Mismatches 39; Indels 12; Gaps 6;
Oy 3 DLSHTPLRRQKYLFDVSMLELSDKEELVGAELRLFRQAPSAPMGPPAGPLHVQLFPCLSPLL 62
Db 112 dlshtplrrqkylfdvstlsdkeelvgadvrlfrqapealappaalalrlp-vapaa 170
Oy 63 LDARTLDPQAGPAGVEVFDVWGLRHQPWKQLCLELRAAW-GELDAGEAEARARGPQQP 121
Db 171 gsaep-gpagaprgvgevdvrglrpqpwkqlclelraawgpeggaedeartpgqqp 229
Oy 122 PPDLRSIGFGRVRPPOERALLVVFTRSQKLNLFAMREQLGSA-EAAGPGAGEGSW- 179
Db 230 ppdlrslgfgrrvrrppqerallvvtfsqrknlfaemreqlgasatevvgpggagewsgp 289
Oy 180 -----PPSGAPDARPLPSPGRRRRRTAFASRHGKRSRLRCSKKPLHVNFKELG 233
Db 290 ppppppppsgtpdaglwspspg-rrrtafasrhgkrsrlrcskskplhvnfkclg 348

```

QY 234 WDDWIIAPLEYAYHCEGVCDPLRSHLEPTNHAIIOTLMSMDPGSTPPSCVPTKLTTP 293
DB 349 WDDWIIAPLEYAYHCEGVCDPLRSHLEPTNHAIIOTLMSMDPGSTPPSCVPTKLTTP 408
QY 294 ISILYIDAGNNVYKQYEDVMVYVESCGR 321
DB 409 ISILYIDAGNNVYKQYEDVMVYVESCGR 436

RESULT 6
AAR78739
ID AAR78739 standard; Protein; 263 AA.
XX
AC AAR78739;
XX
DT 23-NOV-1995 (first entry)
XX
DE Murine mv2 protein..

Bone morphogenetic protein; mv2; tendon; ligament.
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT Misc-difference 54
FT /label= P,T
XX
PN W09516035-A.
XX
PD 15-JUN-1995.
XX
PF 06-DEC-1994; 94WO-US14030.
XX
PR 02-NOV-1994; 94US-0333576.
XX
PR 07-DEC-1993; 93US-0164103.
XX
PR 25-MAR-1994; 94US-0217780.
XX
PA (GENY ) GENETICS INST INC.
PA (HARD ) HARVARD COLLEGE.
XX
PI Celeste AJ, Melton DA, Rosen VA, Thomsen GH, Wolfman NM;
PI Wozney JM;
XX
DR WPI: 1995-224320/29.
DR N-PSDB; AAQ96224.
XX

Bone morphogenetic proteins -12 and -13 and corresp. DNA - used in
compsn. for inducing tendon/ligament-like tissue formation
Example; Page 71-72; 84pp; English.
XX
CC Oligos #6 and #7 (AAQ96218 & AAQ96219) are used as primers for the
CC amplification of a 275 bp DNA probe, the internal 269 bp of which
CC corresp. to nts #607 to #865 of AAQ96207, from the BMP-12 encoding
CC plasmid subclone PCRI-1#2. This probe was radioactively labelled
CC and used to screen a murine genomic library. DNA sequence analysis
CC of one of positively hybridising recombinants named MVR32 indicates
CC that it encodes a portion of the mouse gene corresp. to the PCR
CC product mv2 (murine homolog of the human VL-1 sequence AAQ96213.
CC The partial DNA sequence of this subclone and corresp. AA
CC translation are given in AAQ96224 & AAR78739.
XX
SQ Sequence 263 AA;

Query Match 68.7%; Score 1207.5; DB 16; Length 263;
Best Local Similarity 83.7%; Pred. No. 7.9e-100;
Matches 231; Conservative 6; Mismatches 20; Indels 19; Gaps 4;

QY 46 PAGPLHVQLFPCLSLPDLARTLDPOGAPPAGWEVDFVWQGLRHQPWKQLCIELEAAWGE 105
DB 7 pag-----ptlrgssgtqpr---pag-ksfdvwqglrqpqwkqlcilelraawge 51

```

```

QY 106 LDAGEAEARARCPQPPPPDLRLSGFGRRRVPPPOERALLVVFTRSORKNLFAEMREOLGS 165
DB 52 LDxdtgararqpqppldlrslgfrvrppqerallvfrsqrknlfemheqlgs 111
QY 166 AEAAGPGAGAGSWPPSPGAPDARPWLPSPGRRRRRTAFASRHGKRHGKKSRLRCSKKPL 225
DB 112 aea----agaegscpapspdtswlpspgrrrrrtafasrhgkrhgkksrlrcsrkl 167
QY 226 HVNFKELGWDWIIAPLEYAYHCEGVCDPLRSHLEPTNHAIIOTLMSMDPGSTPPSC 285
DB 168 hvnfkelgwdwiiapleyayhcegvcdplrshleptnhaiqltlnmsmdpgstppsc 227
QY 286 CVPTKLTPISTILYIDAGNNVYKQYEDVMVYVESCGR 321
DB 228 cvptkltplisilyidagnnvvykqyedmvvescgr 263

RESULT 7
AAW26595
ID AAW26595 standard; Protein; 263 AA.
XX
AC AAW26595;
XX
DT 21-JAN-1998 (first entry)
XX
DE Murine BMP-13 homologue fragment.
XX
KW BMP-13; bone morphogenetic protein; mouse; tendon; ligament;
KW wound healing; tissue repair; carpal tunnel syndrome; tendonitis;
KW therapy.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT Misc-difference 54
FT /label= Pro, Thr
FT /note= "encoded by RCC"
FT Misc-difference 247
FT /note= "encoded by GTN"
XX
XX US5658882-A.
XX
XX 19-AUG-1997.
XX
XX 07-DEC-1993; 93US-0164103.
XX
XX 22-DEC-1994; 94US-0362670.
XX
XX 07-DEC-1993; 93US-0164103.
XX
XX 25-MAR-1994; 94US-0217780.
XX
XX 02-NOV-1994; 94US-0333576.
XX
XX (GENY ) GENETICS INST INC.
XX (HARD ) HARVARD COLLEGE.
XX
XX Celeste AJ, Melton DA, Rosen VA, Thomsen GH, Wolfman NM;
XX Wozney JM;
XX
XX WPI: 1997-424270/39.
XX N-PSDB; AAT90397.
XX
XX Inducing tendon and ligament formation using BMP-12, BMP-13 or MP-52
XX - useful for tissue healing and repair, treatment of tendonitis,
XX improving fixation of tendons to bone etc
XX
XX Example 1; Column 69-72; 43pp; English.
XX
XX This polypeptide comprises a fragment of a murine homologue of
XX human bone morphogenetic protein 12 (BMP-13) (see also AAW26591).
XX Its amino acid sequence was deduced from DNA subclone mv2 (see
XX AAT90397), isolated from murine genomic DNA using primers (see
XX AAT90393-94) based on human BMP-12 sequences. Human BMP-13, BMP-12
XX (see AAW26589) and MP52 (see AAW26590) polypeptides are used in a

```

CC claimed method for inducing tendon and ligament formation.

XX Sequence 263 AA;

Query Match 68.7%; Score 1207.5; DB 18; Length 263;
Best Local Similarity 83.3%; Pred. No. 7.9e-100;
Matches 231; Conservative 6; Mismatches 20; Indels 19; Gaps 4;

QY 46 PAGPLHVQLFPCLLDARTLDPOGAPPAGWEVDFVWQGLRHQPKWQKLCLELRAAWGE 105
Db 7 pag-----ptlrgssgtqpr---pag-ksfdvvgglrpqpkqlclelraawge 51
QY 106 LDAGEAEARAGQPPPPDLRLSLGFGRRVRPPOERALLVVFTRSRQKNLFAEMREOLGS 165
Db 52 ldxgdtgarargpqppldlrlslgfgrrvrppqerallvvftrsqrkalfemheqlgs 111
QY 166 AEAAGPAGAGSGWPPSPGAPDARPLSPGRRRRRTAFASRHGKRHKKSLRCSKKPL 225
Db 112 aea-----agaegscpagspdtgswlpsgrrrrrtafasrhgkngkksrlcsrkpl 167
QY 226 HVNFKELGWDWIIAPLEYEAYHCEGVCDPFLRSHLEPTNHAIQTLMNSMDPGSTPPSC 285
Db 168 hvnfkelgwdwiiapleyeayhcegvcdpflrshleptnhaiqltlnmsmdpgstppsc 227
QY 286 CVPTKLTPTISILYIDAGNNVYKQYEDMVVESCGR 321
Db 228 cvptkltptisilyidagnnvvykyedmvvescgr 263

RESULT 8

AAE10985
ID AAE10985 standard; Protein; 263 AA.

XX AAE10985;

XX 18-DEC-2001 (first entry)

XX Murine partial mv2 protein.

XX Mouse; bone morphogenic protein; BMP-12; vulnery; antiinflammatory;
KW analgesic; gene therapy; transforming growth factor-beta; TGF-beta;
KW tissue formation; wound healing; tissue repair; ligament defect;
KW carpal tunnel syndrome; tendonitis; mv2.

XX Mus sp.

XX Key Location/Qualifiers
FT Misc-difference 54 /label= Unknown

FT /note= "Encoded by RCC"

FT Misc-difference 247 /label= Unknown

FT /note= "Encoded by GTN"

XX US6284872-B1.

XX 04-SEP-2001.

XX 28-FEB-1997; 97US-0808324.

XX 22-DEC-1994; 94US-0362670.

XX 07-DEC-1993; 93US-0164103.

XX 25-MAR-1994; 94US-0217780.

XX 02-NOV-1994; 94US-0333576.

XX (GEMV) GENETICS INST INC.

XX (HARD) HARVARD COLLEGE.

XX Celeste AJ, Wozney JM, Rosen VA, Wolfman NM, Thomsen GH;
PI Melton DA;

XX WPI; 2001-588978/66.

DR N-PSDB: AAD18336.

XX New chimeric DNAs, useful for treating tendonitis, carpal tunnel
PT syndrome and other tendon and ligament defects, comprises DNA encoding
PT propeptide linked to DNA encoding bone morphogenetic proteins (BMP)-12,
PT BMP-13 or MP52 .

XX Example 1; Column 71-74; 42pp; English.

XX The invention relates to a chimeric DNA comprising a DNA sequence
CC encoding a propeptide from a member of the transforming growth factor
CC (TGF)-beta superfamily of proteins. This DNA is linked to a DNA sequence
CC encoding an amino acid sequence encoding a mature polypeptide consisting
CC of Bone Morphogenetic Protein (BMP)-12, BMP-13 or MP52 protein. The DNA
CC sequences are useful for producing proteins which induce tendon/ligament
CC like tissue formation, and for isolating and cloning further DNA
CC sequences encoding BMP-12 related proteins with similar activity. The
CC proteins are useful for the induction of tendon/ligament-like tissue
CC formation, wound healing, ligament and other tissue repair, augmenting
CC the activity of bone morphogenetic proteins, and for treating tendonitis,
CC carpal tunnel syndrome and other tendon and ligament defects. The
CC present sequence is murine partial mv2 protein which is homologous to
CC human BMP-12 or VL-1 sequences of the invention.

XX Sequence 263 AA;

Query Match 68.4%; Score 1202.5; DB 22; Length 263;

Best Local Similarity 83.3%; Pred. No. 2.2e-99;

Matches 230; Conservative 6; Mismatches 21; Indels 19; Gaps 4;

QY 46 PAGPLHVQLFPCLLDARTLDPOGAPPAGWEVDFVWQGLRHQPKWQKLCLELRAAWGE 105
Db 7 pag-----ptlrgssgtqpr---pag-ksfdvvgglrpqpkqlclelraawge 51

QY 106 LDAGEAEARAGQPPPPDLRLSLGFGRRVRPPOERALLVVFTRSRQKNLFAEMREOLGS 165
Db 52 ldxgdtgarargpqppldlrlslgfgrrvrppqerallvvftrsqrkalfemheqlgs 111

QY 166 AEAAGPAGAGSGWPPSPGAPDARPLSPGRRRRRTAFASRHGKRHKKSLRCSKKPL 225
Db 112 aea-----agaegscpagspdtgswlpsgrrrrrtafasrhgkngkksrlcsrkpl 167

QY 226 HVNFKELGWDWIIAPLEYEAYHCEGVCDPFLRSHLEPTNHAIQTLMNSMDPGSTPPSC 285
Db 168 hvnfkelgwdwiiapleyeayhcegvcdpflrshleptnhaiqltlnmsmdpgstppsc 227

QY 286 CVPTKLTPTISILYIDAGNNVYKQYEDMVVESCGR 321

Db 228 cvptkltptisilyidagnnvvykyedmvvescgr 263

RESULT 9

AAR40800

ID AAR40800 standard; Protein; 401 AA.

XX AAR40800;

XX 11-FEB-1994 (first entry)

XX TGF-beta-like clone MP-52 protein.

XX Human; transforming growth factor; beta; TGF-beta; pharmaceutical;
KW bone; cartilage; tooth; wound repair; immunosuppressor;
KW organ transplant; cosmetic surgery; antibody; diagnosis.

XX Homo sapiens.

XX WO9316099-A.

XX 19-AUG-1993.

XX 12-FEB-1993; 93WO-EP003350.

XX PR 12-FEB-1992; 92EP-0102324.
XX PA (BIOP-) BIOPHARM GES BIOTECHNOLOGISCHEN ENTWICKL.
XX PI Hoetten G, Neidhardt H;
XX DR WPI; 1993-272824/34.
XX DR N-PSDB; AAQ47709.
XX PT New transforming growth factor-beta family proteins and DNA -
PT used in tissue and wound repair, in treatment of bone, cartilage
PT and tooth defects, and antibodies for diagnosis
XX PT Claim 11; Page 19; 29pp; English.
XX CC The sequences given in AAR40800 and AAR45447 represent fragments of
CC embryo and liver derived human transforming growth factor-beta
CC (TGF-beta) respectively. The full length protein may be used in a
CC pharmaceutical composition for the treatment of various bone, cartilage
CC or tooth defects and in tissue and wound repair processes. These
CC proteins may also be used as immunosuppressors in organ transplants and
CC in cosmetic surgery. Antibodies raised against these proteins may be
CC used for diagnostic purposes.
XX SQ Sequence 401 AA;

Query Match 43.9%; Score 771; DB 14; Length 401;
Best Local Similarity 51.1%; Pred. No. 1.3e-60;
Matches 166; Conservative 46; Mismatches 61; Indels 52; Gaps 12;

QY 9 LRKQYLFVDSMLSDKEELVCAELRLFRQAPS-----APWPPAGPLHVOLFCLSL--- 59
DB 117 VRKQYVFDISAL-ekdgligaelrlrkpsdtakpaapgggaaql--klsscpsgrq 173
QY 60 -PLLLDARTLDPQGAPPAGWEVDFVWQGLRH-OPWKQLCLELRAAWGELDAGEAERARG 117
DB 174 PASLIDVRSV--pgldsgwvfdiwlfrnknsaqiclele-aw---ergra----- 221
QY 118 PQOPPPDLRLSGFGRVRPPQERALLVVTFRSQRKNL-FAEMREQLGSAEAAGPGAGAE 176
DB 222 -----vdlrglgfdrarqvhkalfivgrtkrdlffneikarsgqdk----- 268
QY 177 GSWPPPGAPDARPLSPGRRRTAFASRHGKRHKSKRLCSKPLHVNFKELGWDD 236
DB 269 -----vyeylfsq-rrkraplratrgkrpsknkarscrkalhvnfdmgwdd 316
DB 237 WIIAPLEYAYHCEGVGDFPLRLSHLEPTNHAIIQTLMNSMDPGSTPPSCCVPTKLTPISI 296
DB 317 WIIAPLEYAFHCEGLCEFLPRLSHLEPTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISI 376
QY 297 LYIDAGNNVYKQYEDMVVESCGR 321
DB 377 lfidsannvvykyedmvvescgr 401

RESULT 10
AAR69600
ID AAR69600 standard; Protein: 501 AA.
XX AC AAR69600;
XX DT 10-OCT-1995 (first entry)
XX DE New TGF-beta family member - MP-52 protein sequence.
KW Transforming growth factor-beta family; mitogenic; differentiation;
KW treatment; prevention; disease; bone; cartilage; connective tissue;
KW skin; mucosa; epithelium; dental tissue; wound healing; osteoporosis;
KW tissue regeneration; arthritis; ss.
OS Homo sapiens.

XX KEY Location/Qualifiers
FT Peptide 382
FT /label= mature protein
XX PN WO9504819-A.
XX PD 16-FEB-1995.
XX PF 09-AUG-1994; 94WO-EP02630.
XX PR 10-AUG-1993; 93DE-4326829.
XX PR 25-MAY-1994; 94DE-4418222.
XX PR 09-JUN-1994; 94DE-4420157.
XX PA (BIOP-) BIOPHARM GES BIOTECHNOLOGISCHEN ENTWICKL.
XX PI Hoetten G, Neidhardt H, Paulista M, Hoetten G;
XX WPI; 1995-090897/12.
XX DR N-PSDB; AAQ83695.
XX PT New DNA encoding a new member of the TGF beta family - and
PT related vectors, host cells etc., has mitogenic and
PT differentiation inducing activity, e.g. for treating or
PT preventing diseases of bone and cartilage etc.
XX PS Claim 6; Page 36; 51pp; German.
XX CC The amino acid sequence of a novel member of the transforming growth
CC factor-beta (TGF-b) family named MP-52. The gene encodes a protein
CC of 501 amino acids (AA). The protein, or at least the mature protein,
CC has mitogenic and/or differentiation inducing properties useful in
CC the treatment or prevention of diseases of bone, cartilage, connective
CC tissue, skin, mucosa, epithelium or dental tissue. The protein can also
CC be used for wound healing and tissue regeneration e.g. in osteoporosis
CC and arthritis.
XX SQ Sequence 501 AA;

Query Match 43.9%; Score 771; DB 16; Length 501;
Best Local Similarity 51.1%; Pred. No. 1.7e-60;
Matches 166; Conservative 46; Mismatches 61; Indels 52; Gaps 12;

QY 9 LRKQYLFVDSMLSDKEELVCAELRLFRQAPS-----APWPPAGPLHVOLFCLSL--- 59
DB 217 VRKQYVFDISAL-ekdgligaelrlrkpsdtakpaapgggaaql--klsscpsgrq 273
QY 60 -PLLLDARTLDPQGAPPAGWEVDFVWQGLRH-OPWKQLCLELRAAWGELDAGEAERARG 117
DB 274 PASLIDVRSV--pgldsgwvfdiwlfrnknsaqiclele-aw---ergra----- 321
QY 118 PQOPPPDLRLSGFGRVRPPQERALLVVTFRSQRKNL-FAEMREQLGSAEAAGPGAGAE 176
DB 322 -----vdlrglgfdrarqvhkalfivgrtkrdlffneikarsgqdk----- 368
QY 177 GSWPPPGAPDARPLSPGRRRTAFASRHGKRHKSKRLCSKPLHVNFKELGWDD 236
DB 369 -----vyeylfsq-rrkraplratrgkrpsknkarscrkalhvnfdmgwdd 416
QY 237 WIIAPLEYAYHCEGVGDFPLRLSHLEPTNHAIIQTLMNSMDPGSTPPSCCVPTKLTPISI 296
DB 417 WIIAPLEYAFHCEGLCEFLPRLSHLEPTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISI 476
QY 297 LYIDAGNNVYKQYEDMVVESCGR 321
DB 477 lfidsannvvykyedmvvescgr 501

RESULT 11
AAW36100
ID AAW36100 standard; Protein: 501 AA.

Db	369	- - - - -vveylfsq-rrkraplatrqgkrpsknlkarsckalhvnfkmgwdd	416
Qy	237	WIIAPLEYEAYHCEGVCDFFPLRSHLEPTNHAIQTLMNSMDPGSTPPSCCVPTKLTPISI	296
Db	417	WIIAPLEYEATHCGLCEFPILRSHLEPTNHAIQTLMNSMDPGSTPPSCCVPTKLTPISI	476
Qy	297	LYIDAGNNVYKYQYEDMWVESCGR	321
Db	477	LYIDAGNNVYKYQYEDMWVESCGR	501
RESULT 13			
AAW11900			
ID	AAW11900	standard; Protein; 501 AA.	
XX	AAW11900:		
XX	AAW11900:		
DT	28-OCT-1997	(first entry)	
VV	Human high mol. wt. protein MP52, a growth/differentiation factor.		
AW	Growth factor; differentiation; bone induction; osteoporosis; teeth;		
KW	tooth; dental; joint tissue; cartilage; mucous membrane; skin; nails;		
KW	wound healing; regeneration; skeletal disorder; fracture; dimer.		
XX	Homo sapiens.		
XX	WO9704095-A1.		
XX	06-FEB-1997.		
XX	24-JUL-1996;	96WO-JP02065.	
PF	24-JUL-1995;	95JP-0218022.	
XX	(FARH) HOECHST JAPAN LTD.		
XX	(FARH) HOECHST PHARM & CHEM KK.		
PI	Fujino Y, Kawai S, Kimura M, Matsumoto T, Takahashi M;		
XX	WPI: 1997-132636/12.		
DR	N-PSDB; AAT61412.		
XX	High molecular weight human MP52 growth or differentiation factor -		
PT	promotes bone induction, is useful for treatment and prevention of		
PT	bone disease		
XX	Claim 1; Page 12-16; 25pp; Japanese.		
CC	AAW11900 is a high mol. wt. form of a human growth/differentiation		
CC	factor MP52. MP52 promotes bone induction and is useful for plastic		
CC	reconstructive surgery, cosmetic facial treatment, bone transplant		
CC	and tooth implantation. It is also useful for the treatment and		
CC	prevention of disorders of bone formation, bone, cartilage, joint		
CC	tissue, skin, mucous membranes, nails or teeth; for wound treatment a		
CC	tissue regeneration; and for the treatment of skeletal disorders and		
XX	fractures.		
SQ	Sequence	501 AA;	

```
Query Match      43.9%; Score 771; DB 18; Length 501;
Best Local Similarity 51.1%; Pred. No. 1.7e-60;
Matches 166; Conservative 46; Mismatches 61; Indels 52; Gaps 12;
```

```
Qy    9 LRRKYLEFDVSMLSKEELVGAELELFRQAQS-----APWGPPAGPLHVQLFPCLs--- 59
       :|:|:|:|:| | |:|:|:|:|:|:|:|:| | | | | | | | | |
Db   217 vrkgyvfdisal-ekdglgaelrlrkpsdtakpaapgggraaql--klsscpsgrq 273

Qy    60 -PLLIDARTLDPOGAPPAGNVEFVDWUOGLRH--OPMKQJLCLELRANGELDAGEAERARG 117
       ||| |:| | | | | | | | | | | | | | | | | | | | | |
Db   274 pasllldvrsv--pgldsgvgwfdlwkflfnfknsaqiciclele-aw-----erga ---- 321
```

Qy	118	PQPPPPDLRLSLGRRVRPPQERALLVWTRSORKNL-FAEMREQLGSAEAGPGAGAE	176
Db	322	-----vdllrglgfdaarqvhkalfivgrctkrdlffneikarsggdkdt-----	368
Qy	177	GSWPPSPGADPARWLPSPGRRRRRTAFASRHGKRHCKKSRKSLRCSKKPLHVNFKELGWDD	236
Db	369	-----vyeylfsq-rrkraplratrgqkrpsknkarcskrkalhvnfkdmgwd	416
Qy	237	WIAPLEVEAYHCGVCDFFPLRSHLEPTNHAIQTLMNSMDPGSTPPSCCVPTKLTPISI	296
Db	417	wilapleyeafhcgelcelflrshleptnhaviqtlmnsmdpestptccvtrlpsl	476
Qy	297	LYIDAGNNVYKYQYEDVMVESCGR 321	
Db	477	lfidsannvykyqedmvescgr 501	
RESULT 14			
ID	AAW01799	standard; Protein; 501 AA.	
XX	AAW01799;		
DT	15-OCT-1997	(first entry)	
XX	Human MP52 protein.		
XX	Human; MP52; transforming growth factor; TGF; beta; medicament;		
KW	treatment; prevention; nervous system; disease; neuropathology;		
KW	ageing.		
XX	Homo sapiens.		
OS	DE19525416-A1.		
PN	16-JAN-1997.		
PD	12-JUL-1995; 95DE-1025416.		
XX	12-JUL-1995; 95DE-1025416.		
XX	(BIOP-) BIOPHARM GES BIOTECHNOLOGISCHEN ENTWICKL.		
PA	Bechtold R, Hoetten G, Paulista M, Pohl J, Unsicker K;		
PI	WPI: 1997-078343/08.		
DR	N-PSDB; AAT59405.		
DR	Medicaments contg. protein MP52 - useful for treating neurological disorders		
XX	Claim 2; Pages 12-14; 21pp; German.		
PS	The present sequence is the human MP52 protein, which is		
CC	described in WO 9316099 and 9504819 as a member of the human		
CC	transforming growth factor beta superfamily. Active MP52 can be		
CC	used in a medicament to treat and prevent nervous system diseases,		
CC	and/or to treat neuropathological conditions caused by nervous		
CC	system ageing.		
XX	Sequence 501 AA;		
SQ			
Query Match 43.9%; Score 771; DB 18; Length 501;			
Best Local Similarity 51.1%; Pred. No. 1.7e-60;			
Matches 166; Conservative 46; Mismatches 61; Indels 52; Gaps			
Qy	9	LRRQKYLFDVSMLSDKBELVGAELRFRQAPS-----APWGPAGPLHVQLFPCLSL---	59
Db	217	vrkryvfdisal-ekdglglgaelrirkkpsdtakpaaggggraaql--klsscpgsq	273
Qy	60	-PLLLDARTLDPGAGPAGWEVDFVWQGLRH-QPMKOLCLELRAANGELDAGEAERARG	117

Sequence 501 AA;

Query Match	43.9%	Score 771;	DB 18;	Length 501;
Best Local Similarity	51.1%;	Pred. No. 1.7e-60;		
Matches 166: Conservative	46;	Mismatches 61;	Indels 52;	Gaps 12;

```
Qy      9 LRRKYFLFDVSMLSKDELVGAEURLFRQAPS-----APWPPAGPLHWQLFPCULS---59  
       :|::||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::  
Db     217 vrkryvfdisal-ekgdllgaeirlrkpsdtakpaapgggaaql--klsscpsgrq 273  
  
Qy     60 -PLLLDARTLDPQGAPGAPGVFVDWGGLRH-QPWKLCLLELRANGELDAGEAERARG 117  
       |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::
```

Db 274 paslldvrsv--pgldsgwevdiwklfnknsaqclclele-aw---ergra----- 321
QY 118 POQPPPDLSLGFGRVRPPQERALLVFTSRQKNL-FAEMREOLGSAEAGPGAGAE 176
Db 322 -----vdrlgldgraaarqvhkalfvgrtkkrdlfnfkarsgqdkl----- 368
QY 177 GSWPPPGAPDARPLPSPGRRRRRTAFASRHGKSRKSLRCLPLHVNFKELGWDD 236
Db 369 -----vyeylfsq-rrkraplratrggkrpsknlkarsckalhvnfkdmgwd 416
QY 237 WIIAPLEYAYHCEGVCDPPLRSHLEPTNHAIQTLMNSMDPGSTPPSCCVPTKLTPI 296
Db 417 wiiapleyeafhceglcfprshleptnhaviqtlmnsmdpestptccvptrlspisi 476
QY 297 LYIDAGNNVYKQYEDMVVESCGR 321
Db 477 lfidsannvvykyedmvvescgr 501

RESULT 15

AAW12770
AAW12770 standard; Protein; 501 AA.
AAW12770;
11-MAY-1997 (first entry)
Human bone morphogenic factor MP52 Arg.
Bone morphogenic factor; MP52 Arg; bone; cartilage; skin;
connective tissue; mucous membrane; epithelium; teeth;
wound healing; vulnery; tissue regeneration; osteoporosis;
bone fracture; dental implant; osteoblast.
Homo sapiens.
Key Location/Qualifiers
Peptide 1..27
/label= Sig_peptide
Cleavage-site 380..381
/note= "sequencing suggests MP52 Arg is processed
proteolytically at Arg380-Arg381"
Cleavage-site 381..382
/note= "alternative cleavage site at Arg381-Ala382"
Mat_protein 381..501
/label= Mat_protein
/note= "mature MP52 Arg preferred for use in
compsns. of the invention"

WO9706254-A1.
20-FEB-1997.
02-AUG-1996; 96WO-EP03427.
03-AUG-1995; 95EP-0112241.
(BIOP-) BIOPHARM GES BIOTECHNOLOGISCHEN ENTWICKLUNG.
Fujino Y, Kawai S, Kimura M, Matsumoto T, Takahashi M;
WPI: 1997-154261/14.
N-PSDB; AAT59729.
New human bone morphogenic factor, MP52 Arg - used in the treatment
of osteoporosis and bone fracture, and for promoting bone regrowth
Claim 1; Page 12-15; 26pp; English.
Novel human bone morphogenic factor MP52 Arg (AAW12770) is a growth
factor that induces formation of cartilage from undifferentiated
mesenchymal cells and which stimulates the differentiation and
maturation of osteoblasts. It is effective for treating/preventing

CC bone diseases caused by abnormal bone metabolism such as
CC osteoporosis. It also accelerates the healing of bone fractures,
CC and is useful for orthopaedic reconstruction, bone transplantation,
CC and dental therapeutics because of its bone morphogenetic activity.
CC It is also effective for preventing/treating cartilage, skin,
CC connective tissue, mucous membrane, teeth and epithelial disorders.
CC Recombinant MP52 Arg can be produced in host (e.g. CHO) cells
CC utilising an isolated DNA sequence (AAT59729) in plasmid pKSS99.
XX
SQ Sequence 501 AA;
Query Match 43.9%; Score 771; DB 18; Length 501;
Best Local Similarity 51.1%; Pred. No. 1.7e-60;
Matches 166; Conservative 46; Mismatches 61; Indels 52; Gaps 12;
QY 9 LRRQKLYFDVSMLSKDELVEAGELRLFRQAPS-----APWPPAGPLRHVQLFPCLSL--- 59
Db 217 vrkqrvfdisal-ekdgilgaelrilkkpsdtakpaapgggraql--klsscpgrq 273
QY 60 -PLLDARTLDPOGAPPAGWEVDFVWQGLRH-OPWKQLCLELRAWGLDAGEAEARARG 117
Db 274 paslldvrsv--pgldsgwevdiwklfnknsaqclclele-aw---ergra----- 321
QY 118 POQPPPDLSLGFGRVRPPQERALLVFTSRQKNL-FAEMREOLGSAEAGPGAGAE 176
Db 322 -----vdrlgldgraaarqvhkalfvgrtkkrdlfnfkarsgqdkl----- 368
QY 177 GSWPPPGAPDARPLPSPGRRRRRTAFASRHGKSRKSLRCLPLHVNFKELGWDD 236
Db 369 -----vyeylfsq-rrkraplratrggkrpsknlkarsckalhvnfkdmgwd 416
QY 237 WIIAPLEYAYHCEGVCDPPLRSHLEPTNHAIQTLMNSMDPGSTPPSCCVPTKLTPI 296
Db 417 wiiapleyeafhceglcfprshleptnhaviqtlmnsmdpestptccvptrlspisi 476
QY 297 LYIDAGNNVYKQYEDMVVESCGR 321
Db 477 lfidsannvvykyedmvvescgr 501

Search completed: October 3, 2002, 15:38:39
Job time: 320 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 3, 2002, 15:39:08 ; Search time 23.43 seconds
(without alignments)
334.640 Million cell updates/sec

Title: US-09-945-182-26

Perfect score: 1757

Sequence: 1 NSDSLSTPLRRQKYLFDVSM.....GNVYKQYEDMVESCGCR 321

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

al number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents_AA.*

- 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1757	100.0	321	1	US-08-362-670B-26
2	1757	100.0	321	3	US-08-333-576C-26
3	1757	100.0	321	4	US-08-808-324-26
4	1757	100.0	321	5	PCT-US94-14030A-26
5	1202.5	68.4	263	1	US-08-362-670B-32
6	1202.5	68.4	263	3	US-08-333-576C-32
7	1202.5	68.4	263	4	US-08-808-324-32
8	1202.5	68.4	263	5	PCT-US94-14030A-32
9	771	43.9	401	3	US-08-289-222E-3
10	771	43.9	401	4	US-09-054-526B-3
11	771	43.9	501	2	US-08-288-508C-2
12	765	43.5	388	1	US-08-362-670B-34
13	765	43.5	388	3	US-08-333-576C-34
14	765	43.5	388	5	US-08-808-324-34
15	765	43.5	388	5	PCT-US94-14030A-34
16	765	43.5	495	1	US-08-455-559-10
17	765	43.5	495	5	US-09-145-060-10
18	765	43.5	495	5	PCT-US94-00657-10
19	731	41.6	134	1	US-08-581-529B-6
20	731	41.6	134	3	US-09-097-616-6
21	731	41.6	134	5	PCT-US94-07762-6
22	691.5	39.4	294	1	US-08-362-670B-2
23	691.5	39.4	294	3	US-08-333-576C-2
24	691.5	39.4	294	4	US-08-808-324-2
25	691.5	39.4	294	5	PCT-US94-14030A-2
26	661	37.6	119	1	US-08-581-529B-7
27	661	37.6	119	3	US-09-097-616-7

28	661	37.6	119	5	PCT-US94-07762-7	Sequence 7, Appl
29	618	35.2	240	1	US-08-362-670B-30	Sequence 30, Appl
30	618	35.2	240	3	US-08-333-576C-30	Sequence 30, Appl
31	618	35.2	240	4	US-08-808-324-30	Sequence 30, Appl
32	618	35.2	240	5	PCT-US94-14030A-30	Sequence 30, Appl
33	584	33.2	411	1	US-08-362-670B-28	Sequence 28, Appl
34	584	33.2	411	3	US-08-333-576C-28	Sequence 28, Appl
35	584	33.2	411	4	US-08-808-324-28	Sequence 28, Appl
36	584	33.2	411	5	PCT-US94-14030A-28	Sequence 28, Appl
37	553	31.5	161	2	US-08-581-528A-6	Sequence 6, Appl
38	553	31.5	161	5	PCT-US94-07799-6	Sequence 6, Appl
39	549	31.2	119	1	US-08-455-559-13	Sequence 13, Appl
40	549	31.2	119	4	US-09-145-060-13	Sequence 13, Appl
41	549	31.2	119	5	PCT-US94-00657-13	Sequence 13, Appl
42	549	31.2	120	1	US-08-362-670B-4	Sequence 4, Appl
43	549	31.2	120	3	US-08-333-576C-4	Sequence 4, Appl
44	549	31.2	120	4	US-08-808-324-4	Sequence 4, Appl
45	549	31.2	120	5	PCT-US94-14030A-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-08-362-670B-26
: Sequence 26, Application US/08362670B
: Patent No. 5658882
: GENERAL INFORMATION:
: APPLICANT: Celeste, Anthony J.
: APPLICANT: Wozney, John
: APPLICANT: Rosen, Vicki A.
: APPLICANT: Wolfman, Neil
: APPLICANT: Thomsen, Gerald H.
: APPLICANT: Melton, Douglas A.
: TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
: NUMBER OF SEQUENCES: 37
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: GENETICS INSTITUTE, INC.
: STREET: 87 CambridgePark Drive
: CITY: Cambridge
: STATE: Massachusetts
: COUNTRY: USA
: ZIP: 02140
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/362,670B
: FILING DATE: December 22, 1994
: CLASSIFICATION: 514
: ATTORNEY/AGENT INFORMATION:
: NAME: Lazar, Steven R.
: REGISTRATION NUMBER: 32,618
: REFERENCE/DOCKET NUMBER: 5202-D
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 617 498-8260
: TELEFAX: 617 876-5851
: INFORMATION FOR SEQ ID NO: 26:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 321 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-362-670B-26

Query Match 100.0% Score 1757; DB 1; Length 321;
Best Local Similarity 100.0%; Pred. No. 1 3e-147;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 NSDSLSTPLRRQKYLFDVSMLSKDEELVGAELRFRQAPSAPMGPPAGPLHVQLFPCLS 60

```

Db 1 NSDLSTPLRQKYLFDVSMLEKEELVGAELRLFRQAPSAPWGPAGPLHVQLFPCCLSP 60
QY 61 LLLDARTLDPOGAPPAGWEVFDVWQGLRHQPWKOLCLLELRAANGELDAGEAARARGPQQ 120
Db 61 LLLDARTLDPOGAPPAGWEVFDVWQGLRHQPWKOLCLLELRAANGELDAGEAARARGPQQ 120
QY 121 PPPDLRLSGFGRVRPPQERALLVVFTRSORKNLFAEMREQLGSAEAGPAGAGSGSWP 180
Db 121 PPPDLRLSGFGRVRPPQERALLVVFTRSORKNLFAEMREQLGSAEAGPAGAGSGSWP 180
QY 181 PPSGAPDARPLPSPGRRRRRTAFASRHGKRGKKSRLRCSKKPLHVNFKELGWDWIIA 240
Db 181 PPSGAPDARPLPSPGRRRRRTAFASRHGKRGKKSRLRCSKKPLHVNFKELGWDWIIA 240
QY 241 PLEYAYHCEGVCDFPLRSHLEPTNHAIQTLNMSMDPGSTPPSCCVPTKLTPTISILYID 300
Db 241 PLEYAYHCEGVCDFPLRSHLEPTNHAIQTLNMSMDPGSTPPSCCVPTKLTPTISILYID 300
QY 301 AGNNVYKQYEDMVVESCGR 321
Db 301 AGNNVYKQYEDMVVESCGR 321

```

RESULT 2

```

US-08-333-576C-26
; Sequence 26, Application US/08333576C
; Patent No. 6027919
; GENERAL INFORMATION:
; APPLICANT: Celeste, Anthony J.
; APPLICANT: Wozney, John
; APPLICANT: Rosen, Vicki A.
; APPLICANT: Wolfman, Neil
; APPLICANT: Thomsen, Gerald H.
; APPLICANT: Melton, Douglas A.
; TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENETICS INSTITUTE, INC.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/333.576C
; FILING DATE: No. 6027919ember 2, 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lazar, Steven R.
; REGISTRATION NUMBER: 32,618
; REFERENCE/DOCKET NUMBER: 5202-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 498-8260
; TELEFAX: 617 876-5851
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 321 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-333-576C-26

```

Query Match 100.0%; Score 1757; DB 3; Length 321;
 Best Local Similarity 100.0%; Pred. No. 1.3e-147;
 Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 NSDLSTPLRQKYLFDVSMLEKEELVGAELRLFRQAPSAPWGPAGPLHVQLFPCCLSP 60
Db 1 NSDLSTPLRQKYLFDVSMLEKEELVGAELRLFRQAPSAPWGPAGPLHVQLFPCCLSP 60
QY 61 LLLDARTLDPOGAPPAGWEVFDVWQGLRHQPWKOLCLLELRAANGELDAGEAARARGPQQ 120
Db 61 LLLDARTLDPOGAPPAGWEVFDVWQGLRHQPWKOLCLLELRAANGELDAGEAARARGPQQ 120
QY 121 PPPDLRLSGFGRVRPPQERALLVVFTRSORKNLFAEMREQLGSAEAGPAGAGSGSWP 180
Db 121 PPPDLRLSGFGRVRPPQERALLVVFTRSORKNLFAEMREQLGSAEAGPAGAGSGSWP 180
QY 181 PPSGAPDARPLPSPGRRRRRTAFASRHGKRGKKSRLRCSKKPLHVNFKELGWDWIIA 240
Db 181 PPSGAPDARPLPSPGRRRRRTAFASRHGKRGKKSRLRCSKKPLHVNFKELGWDWIIA 240
QY 241 PLEYAYHCEGVCDFPLRSHLEPTNHAIQTLNMSMDPGSTPPSCCVPTKLTPTISILYID 300
Db 241 PLEYAYHCEGVCDFPLRSHLEPTNHAIQTLNMSMDPGSTPPSCCVPTKLTPTISILYID 300
QY 301 AGNNVYKQYEDMVVESCGR 321
Db 301 AGNNVYKQYEDMVVESCGR 321

```

RESULT 3

```

US-08-808-324-26
; Sequence 26, Application US/08808324
; Patent No. 6284872
; GENERAL INFORMATION:
; APPLICANT: Celeste, Anthony J.
; APPLICANT: Wozney, John
; APPLICANT: Rosen, Vicki A.
; APPLICANT: Wolfman, Neil
; APPLICANT: Thomsen, Gerald H.
; APPLICANT: Melton, Douglas A.
; TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENETICS INSTITUTE, INC.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/808,324
; FILING DATE: Herewith
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Lazar, Steven R.
; REGISTRATION NUMBER: 32,618
; REFERENCE/DOCKET NUMBER: 5202-D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 498-8260
; TELEFAX: 617 876-5851
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 321 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-808-324-26

```

Query Match 100.0%; Score 1757; DB 4; Length 321;
 Best Local Similarity 100.0%; Pred. No. 1.3e-147;
 Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NSDLSHTPLRRQKYLFDVSMLSKDEELVGAELRFRQAPSAPWGPAGPLHVQLFPCLSP 60
DB 1 NSDLSHTPLRRQKYLFDVSMLSKDEELVGAELRFRQAPSAPWGPAGPLHVQLFPCLSP 60
QY 61 LLLDARTLDPOCAPAGWVEFDVWQGLRHPKQLCLLELRAAWGELDAGEAARARGPOQ 120
DB 61 LLLDARTLDPOCAPAGWVEFDVWQGLRHPKQLCLLELRAAWGELDAGEAARARGPOQ 120
QY 121 PPPDLRLSLGFGRRVRRPQERALLVFTSRQKNLFAEMREQLGSAEAGPGAGAGSWP 180
DB 121 PPPDLRLSLGFGRRVRRPQERALLVFTSRQKNLFAEMREQLGSAEAGPGAGAGSWP 180
QY 181 PPSGADPAPWLPSPGRRRRRTAFASRHGKRSRLRCKKPLHVNFKELGWDWIIA 240
DB 181 PPSGADPAPWLPSPGRRRRRTAFASRHGKRSRLRCKKPLHVNFKELGWDWIIA 240
QY 241 PLEYEAYHCEGVCDPLRSHLEPTNHAIIQTLLNMSMDPGSTPPSCCVPTKLTPISTLYID 300
DB 241 PLEYEAYHCEGVCDPLRSHLEPTNHAIIQTLLNMSMDPGSTPPSCCVPTKLTPISTLYID 300
QY 301 AGNNVYKQYEDMVVESCGR 321
DB 301 AGNNVYKQYEDMVVESCGR 321

RESULT 4
PCT-US94-14030A-26
; Sequence 26, Application PC/TUS9414030A
; GENERAL INFORMATION:
; APPLICANT: GENETICS INSTITUTE, INC.
; APPLICANT: PRESIDENT AND FELLOWS OF HARVARD COLLEGE
; TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENETICS INSTITUTE, INC.
; STREET: 87 Bridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/14030A
; FILING DATE: Berewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/164,103
; FILING DATE: 07-DEC-1993
; APPLICATION NUMBER: US 08/217,780
; FILING DATE: 25-MAR-1994
; APPLICATION NUMBER: US 08/333,576
; FILING DATE: 02-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lazar, Steven R.
; REGISTRATION NUMBER: 32,618
; REFERENCE/DOCKET NUMBER: 5202D-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 498-8260
; TELEFAX: 617 876-5851
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 321 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US94-14030A-26

Query Match 100.0%; Score 1757; DB 5; Length 321;
Best Local Similarity 100.0%; Pred. No. 1.3e-147;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NSDLSHTPLRRQKYLFDVSMLSKDEELVGAELRFRQAPSAPWGPAGPLHVQLFPCLSP 60
DB 1 NSDLSHTPLRRQKYLFDVSMLSKDEELVGAELRFRQAPSAPWGPAGPLHVQLFPCLSP 60
QY 61 LLLDARTLDPOCAPAGWVEFDVWQGLRHPKQLCLLELRAAWGELDAGEAARARGPOQ 120
DB 61 LLLDARTLDPOCAPAGWVEFDVWQGLRHPKQLCLLELRAAWGELDAGEAARARGPOQ 120
QY 121 PPPDLRLSLGFGRRVRRPQERALLVFTSRQKNLFAEMREQLGSAEAGPGAGAGSWP 180
DB 121 PPPDLRLSLGFGRRVRRPQERALLVFTSRQKNLFAEMREQLGSAEAGPGAGAGSWP 180
QY 181 PPSGADPAPWLPSPGRRRRRTAFASRHGKRSRLRCKKPLHVNFKELGWDWIIA 240
DB 181 PPSGADPAPWLPSPGRRRRRTAFASRHGKRSRLRCKKPLHVNFKELGWDWIIA 240
QY 241 PLEYEAYHCEGVCDPLRSHLEPTNHAIIQTLLNMSMDPGSTPPSCCVPTKLTPISTLYID 300
DB 241 PLEYEAYHCEGVCDPLRSHLEPTNHAIIQTLLNMSMDPGSTPPSCCVPTKLTPISTLYID 300
QY 301 AGNNVYKQYEDMVVESCGR 321
DB 301 AGNNVYKQYEDMVVESCGR 321
RESULT 5
US-08-362-670B-32
; Sequence 32, Application US/08362670B
; Patent No. 5658882
; GENERAL INFORMATION:
; APPLICANT: Celeste, Anthony J.
; APPLICANT: Wozney, John
; APPLICANT: Rosen, Vicki A.
; APPLICANT: Wolfman, Neil
; APPLICANT: Thomsen, Gerald H.
; APPLICANT: Melton, Douglas A.
; TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENETICS INSTITUTE, INC.
; STREET: 87 Bridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/362.670B
; FILING DATE: December 22, 1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Lazar, Steven R.
; REGISTRATION NUMBER: 32,618
; REFERENCE/DOCKET NUMBER: 5202-D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 498-8260
; TELEFAX: 617 876-5851
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 263 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-362-670B-32

Query Match 68.4%; Score 1202.5; DB 1; Length 263;
 Best Local Similarity 83.3%; Pred. No. 9.3e-99;
 Matches 230; Conservative 6; Mismatches 21; Indels 19; Gaps 4;

QY 46 PAGPLHVQLFPCSLPLLDARTLDPOGAPPAGWEVFDVWQGLRHQPWKQLCLELRAANGE 105
 DB 7 PAG-----PTLRGSSGTQPR---PAG-KSFDVWQGLRPPQWKQLCLELRAANGE 51

QY 106 LDAGEAEARAGCPQPPDRLSLGFGRRVRPQOERALLVVFTRSORKNLFAEMREQLGS 165
 DB 52 LDAGDGTGARARAGCPQPPDRLSLGFGRRVRPQOERALLVVFTRSORKNLFAEMREQLGS 111

QY 166 AEAAGPAGAGSGWPPSPGAPDARPLSPGRRRRRTAFASRHKRHKKSRLRCSKKPL 225
 DB 112 AEA---AGAGSCPAPSGSDTGSWLPSPGRRRRRTAFASRHKRHKKSRLRCSKKPL 167

QY 226 HVNFKELGWDDWIIAPLEYEAYHCEGVCDFFPLRSHLEPTNHAIQTLMNSMDPGSTPPSC 285
 DB 168 HVNFKELGWDDWIIAPLEYEAYHCEGVCDFFPLRSHLEPTNHAIQTLMNSMDPGSTPPSC 227

QY 286 CVPTKLTPIISILYIDAGNNVYKQYEDMVVESCGR 321
 DB 228 CVPTKLTPIISILYIDAGNNVYKQYEDMVVESCGR 263

RESULT 6
 US-08-333-576C-32
 ; Sequence 32, Application US/08333576C
 ; Patent No. 6027919
 ; GENERAL INFORMATION:
 ; APPLICANT: Celeste, Anthony J.
 ; APPLICANT: Wozney, John
 ; APPLICANT: Rosen, Vicki A.
 ; APPLICANT: Wolfman, Neil
 ; APPLICANT: Thomsen, Gerald H.
 ; APPLICANT: Melton, Douglas A.
 ; TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
 ; NUMBER OF SEQUENCES: 37
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: GENETICS INSTITUTE, INC.
 ; STREET: 87 CambridgePark Drive
 ; CITY: Cambridge
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02140
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/333,576C
 ; FILING DATE: No. 6027919ember 2, 1994
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Lazar, Steven R.
 ; REGISTRATION NUMBER: 32,618
 ; REFERENCE/DOCKET NUMBER: 5202-B
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617 498-8260
 ; TELEFAX: 617 876-5851
 ; INFORMATION FOR SEQ ID NO: 32:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 263 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-333-576C-32

Query Match 68.4%; Score 1202.5; DB 3; Length 263;
 Best Local Similarity 83.3%; Pred. No. 9.3e-99;

Matches 230; Conservative 6; Mismatches 21; Indels 19; Gaps 4;

QY 46 PAGPLHVQLFPCSLPLLDARTLDPOGAPPAGWEVFDVWQGLRHQPWKQLCLELRAANGE 105
 DB 7 PAG-----PTLRGSSGTQPR---PAG-KSFDVWQGLRPPQWKQLCLELRAANGE 51

QY 106 LDAGEAEARAGCPQPPDRLSLGFGRRVRPQOERALLVVFTRSORKNLFAEMREQLGS 165
 DB 52 LDAGDGTGARARAGCPQPPDRLSLGFGRRVRPQOERALLVVFTRSORKNLFAEMREQLGS 111

QY 166 AEAAGPAGAGSGWPPSPGAPDARPLSPGRRRRRTAFASRHKRHKKSRLRCSKKPL 225
 DB 112 AEA---AGAGSCPAPSGSDTGSWLPSPGRRRRRTAFASRHKRHKKSRLRCSKKPL 167

QY 226 HVNFKELGWDDWIIAPLEYEAYHCEGVCDFFPLRSHLEPTNHAIQTLMNSMDPGSTPPSC 285
 DB 168 HVNFKELGWDDWIIAPLEYEAYHCEGVCDFFPLRSHLEPTNHAIQTLMNSMDPGSTPPSC 227

QY 286 CVPTKLTPIISILYIDAGNNVYKQYEDMVVESCGR 321
 DB 228 CVPTKLTPIISILYIDAGNNVYKQYEDMVVESCGR 263

RESULT 7
 US-08-808-324-32
 ; Sequence 32, Application US/08808324
 ; Patent No. 6284872
 ; GENERAL INFORMATION:
 ; APPLICANT: Celeste, Anthony J.
 ; APPLICANT: Wozney, John
 ; APPLICANT: Rosen, Vicki A.
 ; APPLICANT: Wolfman, Neil
 ; APPLICANT: Thomsen, Gerald H.
 ; APPLICANT: Melton, Douglas A.
 ; TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
 ; NUMBER OF SEQUENCES: 35
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: GENETICS INSTITUTE, INC.
 ; STREET: 87 CambridgePark Drive
 ; CITY: Cambridge
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02140
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/808,324
 ; FILING DATE: Herewith
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Lazar, Steven R.
 ; REGISTRATION NUMBER: 32,618
 ; REFERENCE/DOCKET NUMBER: 5202-D
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617 498-8260
 ; TELEFAX: 617 876-5851
 ; INFORMATION FOR SEQ ID NO: 32:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 263 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-808-324-32

Query Match 68.4%; Score 1202.5; DB 4; Length 263;
 Best Local Similarity 83.3%; Pred. No. 9.3e-99;
 Matches 230; Conservative 6; Mismatches 21; Indels 19; Gaps 4;

QY 46 PAGPLHVQLFPCSLPLLDARTLDPOGAPPAGWEVFDVWQGLRHQPWKQLCLELRAANGE 105

[illegible]

```

1  ULT 8
2  PCT-US94-14030A-32
3  Sequence 32, Application PC/TUS9414030A
4  GENERAL INFORMATION:
5  APPLICANT: GENETICS INSTITUTE, INC.
6  APPLICANT: PRESIDENT AND FELLOWS OF HARVARD COLLEGE
7  TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
8  NUMBER OF SEQUENCES: 35
9  CORRESPONDENCE ADDRESS:
10 ADDRESSEE: GENETICS INSTITUTE, INC.
11 STREET: 87 CambridgePark Drive
12 CITY: Cambridge
13 STATE: Massachusetts
14 COUNTRY: USA
15 ZIP: 02140
16 COMPUTER READABLE FORM:
17 MEDIUM TYPE: Floppy disk
18 COMPUTER: IBM PC compatible
19 OPERATING SYSTEM: PC-DOS/MS-DOS
20 SOFTWARE: PatentIn Release #1.0, Version #1.25
21 CURRENT APPLICATION DATA:
22 APPLICATION NUMBER: PCT/US94/14030A
23 FILING DATE: Herewith
24 CLASSIFICATION:
25 PRIOR APPLICATION DATA:
26 APPLICATION NUMBER: US 08/164,103
27 FILING DATE: 07-DEC-1993
28 APPLICATION NUMBER: US 08/217,780
29 FILING DATE: 25-MAR-1994
30 APPLICATION NUMBER: US 08/333,576
31 FILING DATE: 02-NOV-1994
32 ATTORNEY/AGENT INFORMATION:
33 NAME: Lazar, Steven R.
34 REGISTRATION NUMBER: 32,618
35 REFERENCE/DOCKET NUMBER: 5202D-PCT
36 TELECOMMUNICATION INFORMATION:
37 TELEPHONE: 617 498-8260
38 TELEFAX: 617 876-5851
39 INFORMATION FOR SEQ ID NO: 32:
40 SEQUENCE CHARACTERISTICS:
41 LENGTH: 263 amino acids
42 TYPE: amino acid
43 TOPOLOGY: linear
44 MOLECULE TYPE: protein
45 PCT-US94-14030A-32

```

```
Query Match      68.4%; Score 1202.5; DB 5; Length 263;
Best Local Similarity 83.3%; Pred. No. 9,3e-99;
Matches 230; Conservative 6; Mismatches 21; Indels 19; Gaps 4;
```

```

Db      7  PAG-----PTURGSSGTQPR---PAG-KSFVDWGLRPPQPHKQLCLLELRANGE 51
Qy      106  LDAGEAEARAGPOOPPPDLRSIFGRRYRPPQERALLVYVFTSRQKNLFAEMREQLGS 165
Db      52  LDXGDTGARAGPOOPPLDLRSIFGRRYRPPQERALLVYVFTSRQKNLFTEMHEQLGS 111
Qy      166  AEAAGPAGAGSWPPSPSGAPDARPLPSGRRRRRTAFASRHKGRHGKKSRLRCSKKPL 225
Db      112  AEA-----AGAEGSCAPSPGSDTGSWLPSPGRRRRRTAFASRHKGRHGKKSRLRCSRKPL 167
Qy      226  HVNFKELGWDWIIAPLEYEAYHCEGVCDFPLRSHLEPTNHAIIQTLMNSMDPGSTPPSC 285
Db      168  HVNFKELGWDWIIAPLEYEAYHCEGVCDFPLRSHLEPTNHAIIQTLMNSMDPGSTPPSC 227
Qy      286  CVPTKLPISILYIDAGNNVYKQYEDMVVESCGR 321
Db      228  CVPTKLPISILYIDAGNNVYKQYEDMVVESCGR 263

RESULT 9
US-08-289-222E-3
: Sequence 3, Application US/08289222E
: Patent No. 6120760
: GENERAL INFORMATION:
: APPLICANT: HOTTEN, GERTRUD
: APPLICANT: NEIDHARDT, HELGE
: APPLICANT: BECHTOLD, ROLF
: APPLICANT: POHL, JENS
: TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS OF THE TGF-B
: TITLE OF INVENTION: FAMILY
: NUMBER OF SEQUENCES: 53
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: NIKAIIDO, MARCELSTEIN, MURRAY & ORAM
: STREET: 655 FIFTEENTH STREET, N. W., G STREET LOBBY,
: STREET: SUITE 330
: CITY: WASHINGTON
: STATE: DC
: COUNTRY: USA
: ZIP: 20005-5701
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/289,222E
: FILING DATE: 25-AUG-1999
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/289,222
: FILING DATE: 12-AUG-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: DE P 44 23 190.3
: FILING DATE: 07-JUL-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: EPO 92102324.8
: FILING DATE: 12-FEB-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/EP93/00350
: FILING DATE: 12-FEB-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: KITTS, MONICA CHIN
: REGISTRATION NUMBER: 36,105
: REFERENCE/DOCKET NUMBER: P564-9021
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202/638-5000
: TELEFAX: 202/638-4810
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 401 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear

```


Search completed: October 3, 2002, 15:39:09
Job time: 235 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 3, 2002, 15:39:44 ; Search time 29.81 Seconds
(without alignments)
1034.709 Million cell updates/sec

Title: US-09-945-182-26
Perfect score: 1757
Sequence: 1 NSDLSHTPLRRQKYLFDVSM.....GNVVYKQYEDMVVESCGR 321

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues
Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 71.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1368	77.9	436	2 B55452	cartilage-derived
2	771	43.9	501	2 JC2347	growth/differentia
3	765	43.5	495	2 S43294	bone morphogenetic
4	762	43.4	501	2 A55452	cartilage-derived
5	691	39.3	125	2 S43295	bone morphogenetic
6	549	31.2	151	2 S43296	bone morphogenetic
7	426.5	24.3	398	2 JH0588	bone morphogenetic
8	425.5	24.2	398	2 JH0587	bone morphogenetic
9	418.5	23.8	405	2 I50608	bone morphogenetic
10	406.5	23.1	408	1 BMH04	bone morphogenetic
11	405.5	23.1	452	2 I49542	bone morphogenetic
12	405.5	23.1	461	2 S52408	SPDVR1 protein - s
13	401	22.8	393	2 S37073	bone morphogenetic
14	401	22.8	420	2 I49541	bone morphogenetic
15	396.5	22.6	454	1 BMH05	bone morphogenetic
16	396	22.5	408	2 S38343	bone morphogenetic
17	395	22.5	394	2 S45355	bone morphogenetic
18	391	22.3	408	2 JH0801	bone morphogenetic
19	388.5	22.1	396	1 BMH02	bone morphogenetic
20	387	22.0	430	2 JQ1184	osteogenic protein
21	386	22.0	431	1 BMH07	bone morphogenetic
22	385.5	21.9	402	2 A45056	osteogenic protein
23	384	21.9	313	2 I51284	bone morphogenetic
24	384	21.9	426	2 JH0690	bone morphogenetic
25	379	21.6	400	2 A49147	bone morphogenetic
26	378	21.5	408	2 S58791	bone morphogenetic
27	377	21.5	401	2 JH0689	bone morphogenetic
28	375	21.3	353	2 I50607	bone morphogenetic
29	369	21.0	588	2 A26158	decapentaplegic pr

30 362.5 20.6 354 2 S29718 gene nodal protein
31 360 20.5 510 2 A54798 Vg-1-related prote
32 351 20.0 513 1 BMH06 bone morphogenetic
33 343 19.5 365 2 T43286 cat-1 protein - Ca
34 339.5 19.3 427 2 A40735 TGF beta homolog d
35 334 19.0 207 2 S37618 vgr protein - rat
36 332 18.9 455 2 A43918 TGF-beta-related p
37 328 18.7 478 2 JC4838 bone morphogenetic
38 324.5 18.5 360 2 A29619 Vg1 embryonic grow
39 312 17.8 476 2 JC4646 bone morphogenetic
40 308 17.5 372 2 C39364 GDF-1 embryonic gr
41 299 17.0 366 2 A46607 growth/differentia
42 293 16.7 472 1 BMH03 bone morphogenetic
43 292.5 16.6 426 1 B24248 inhibit beta-A cha
44 290 16.5 366 2 A5402 transforming growt
45 289.5 16.5 424 1 WFPGBA inhibit beta-A cha

ALIGNMENTS

RESULT 1

B55452 cartilage-derived morphogenetic protein 2 precursor - bovine (fragment)

C:Species: Bos primigenius taurus (cattle)
C:Date: 10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change 26-May-2000

C:Accession: B55452

R:Chang, S.C.; Hoang, B.; Thomas, J.T.; Vukicevic, S.; Luyten, F.P.; Ryba, N.J.P.; K

J. Biol. Chem. 269, 28227-28234, 1994

A:Title: Cartilage-derived morphogenetic proteins. New members of the transforming g

A:Reference number: A55452; MUID:95050604

A:Accession: B55452

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-436 <CHA>

A:Cross-references: GB:U13661; NID:g632489; PIDN:AAA61416.1; PID:g632490

C:Superfamily: inhibit

Query Match 77.9%; Score 1368; DB 2; Length 436;

Best Local Similarity 81.7%; Pred. No. 2e-95;

Matches 268; Conservative 9; Mismatches 39; Indels 12; Gaps 6;

QY 3 DLSHTPLRRQKYLFDVSMISDKELVGAELRFRQAPSAPWGPAGPLHVQLFPCLSPLL 62
DB 112 DLSHTPLRRQKYLFDVSTLSKDELVGADVRLFRQAPALAPPAAALRALP-VAPAA 170
QY 63 LDARTLDPOGAPPAGWEVDVWGQHRQKQLCLRLAAW-GELDAGEAARAGPOOP 121
DB 171 GSAEP-GPAGAPRPGWEVDVWRGLRQPKWQLCLRLAAWGGEPGAAEDEARTPGPOOP 229
QY 122 PPDLSLGLGRRVRPQERALLVFTSRQKNLFAEMREQLGSA-EAAGPGAGAGSGW- 179
DB 230 PPDLSLGLGRRVRPQERALLVFTSRQKTLFEMREQLGSATEVVGSGGAGSGP 289
QY 180 -----PPPSGAPDAPWLPSPGRRRRRTAFASRHGKRHKSRKSLRCSKKPLHVNFKELG 233
DB 290 PPPPPPPPSGTPDAGLWSPG-RRRTAFASRHGKRHKSRKSLRCSKKPLHVNFKELG 348
QY 234 WDDWIIAPLEYAYHCEGVCDFFLRSHLEPTNHAIIOTLMNSMDPGSTPPSCCVPTKLTP 293
DB 349 WDDWIIAPLEYAYHCEGVCDFFLRSHLEPTNHAIIOTLMNSMDPGSTPPSCCVPTKLTP 408
QY 294 ISILYIDAGNNVYKQYEDMVVESCGR 321
DB 409 ISILYIDAGNNVYNEYEEMVESCGR 436

RESULT 2

JC2347 growth/differentiation factor 5 - human

C:Species: Homo sapiens (man)

C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 17-Mar-2000

C:Accession: JC2347

R:Hoetten, G.; Neidhardt, H.; Jacobowsky, B.; Pohl, J.

Biochem. Biophys. Res. Commun. 204, 646-652, 1994

A:Title: Cloning and expression of recombinant human growth/differentiation factor 5.

A:Reference number: JC2347; MUID:95071375

A:Accession: JC2347

A:Molecule type: DNA

A:Residues: 1-501 <HO>

A:Cross-references: GB:X80915; NID:g671524; PIDN:CAA56874.1; PID:g671525

C:Genetics:

A:Gene: GDB:BMP9

A:Cross-references: GDB:433948

A:Introns: 211/1

C:Superfamily: inhibin

C:Keywords: glycoprotein

F:189/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:381-382/Cleavage site: Arg-Ala (unidentified proteinase) #status predicted

Query Match 43.9%; Score 771; DB 2; Length 501;
Best Local Similarity 51.1%; Pred. No. 1.6e-50;
Matches 166; Conservative 46; Mismatches 61; Indels 52; Gaps 12;

Qy 9 LRRQKYLFDVSMDSKDELVAELRLFRQAPS-----APWGPAGPLHVQLFPCLSL--- 59
Db 217 VRKQRYVFDISAL-EKDGLLGAELRLRKKPSDTAKPAAPGGGAAQL--KLSSCPSGRQ 273
Qy 60 -PLLDARTLDPQAGPAGWEVDVWQGLRH-OPWKQLCLLELAANGELDAGEAEARAG 117
Db 274 PASLLDVRSV--PGLDGSWEVDFINKLFRNFKNSAQLCLE-AW---ERGRA----- 321
Qy 118 POQPPPPDLRLSGFGRVRPPQERALLVFTSRQKNL-FAEMREOLGSAEAGPGAGAE 176
Db 322 -----VDLRGLGFDRAARQVHEKALFLVFGTRKKRDLFFNEIKARSGQDDKT----- 368
Qy 177 GSWPPPGAPDARPLSPGRRRRRTAFASRHGKRRHKKSLRCSKKPLHVNFKELGWDD 236
Db 369 -----VVEYLFSQ--RRKRRAPLATROGKRPSKRLKARCSRKALHVNFKDGMGDD 416
Qy 237 WIIAPLEYEAYHCEGVCDFFPLRSHLEPTNHAIQTLMNSMDPGSTPPSCCVPTKLTPISI 296
Db 417 WIIAPLEYEAFHCEGLCEFPPLRSHLEPTNHAVIOTLMNSMDPESTPTCCVPTRLSPISI 476
Qy 297 LYIDAGNNVYKQYEDMVVESCGR 321
Db 477 LFIDSANNVYKQYEDMVVESCGR 501

RESULT 3

43294

C:One morphogenetic protein-related protein (GDF5) - mouse

C:Species: Mus musculus (house mouse)

C>Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 17-Mar-2000

C:Accession: S43294

R:Storm, E.E.; Huynh, T.V.; Copeland, N.G.; Jenkins, N.A.; Kingsley, D.M.; Lee, S.J.

Nature 368, 639-643, 1994

A:Title: Limb alterations in brachypodism mice due to mutations in a new member of the

A:Reference number: S43294; MUID:94195427

A:Accession: S43294

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-495 <STO>

A:Cross-references: GB:008337; NID:9488461; PIDN:AAA18778.1; PID:g488462

C:Superfamily: inhibin

Query Match 43.5%; Score 765; DB 2; Length 495;
Best Local Similarity 50.5%; Pred. No. 4.5e-50;
Matches 163; Conservative 50; Mismatches 62; Indels 48; Gaps 12;

Qy 9 LRRQKYLFDVSMDSKDELVAELRLFRQAP---SAPWGPAGPL-HVQLFPCLSL---P 60
Db 211 VRKQRYVFDISAL-EKDGLLGAELRLRKKPLDVAKPAPSGRVAQLKLSSCPSGRQPA 269

Qy 61 LLLDARTLDPQAGPAGWEVDVWQGLRH-OPWKQLCLLELAANGELDAGEAEARAGPQ 119
Db 270 ALLDVRSV--PGLDGSWEVDFINKLFRNFKNSAQLCLE-FAEMREOLGSAEAGPGAGAE 315
Qy 120 QPPPPDLRLSGFGRVRPPQERALLVFTSRQKNL-FAEMREOLGSAEAGPGAGAE 178
Db 316 ---VDLRGLGFDRAARQVHEKALFLVFGTRKKRDLFFNEIKARSGQDDKT----- 362
Qy 179 WPPPGAPDARPLSPGRRRRRTAFASRHGKRRHKKSLRCSKKPLHVNFKELGWDDWI 238
Db 363 -----VVEYLFSQ--RRKRRAPLATROGKRPSKRLKARCSRKALHVNFKDGMGDDWI 412
Qy 239 IAPLEYEAYHCEGVCDFFPLRSHLEPTNHAIQTLMNSMDPGSTPPSCCVPTKLTPISI 298
Db 413 IAPLEYEAFHCEGLCEFPPLRSHLEPTNHAVIOTLMNSMDPESTPTCCVPTRLSPISI 472
Qy 299 IDAGNNVYKQYEDMVVESCGR 321
Db 473 IDSANNVYKQYEDMVVESCGR 495

RESULT 4

A55452

C:cartilage-derived morphogenetic protein 1 precursor - human

C:Species: Homo sapiens (man)

C>Date: 10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change 17-Mar-2000

C:Accession: A55452

R:Chang, S.C.; Hoang, B.; Thomas, J.T.; Vukicevic, S.; Luyten, F.P.; Ryba, N.J.P.; J.

J. Biol. Chem. 269, 28227-28234, 1994

A:Title: Cartilage-derived morphogenetic proteins. New members of the transforming

A:Reference number: A55452; MUID:95050604

A:Accession: A55452

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-501 <CHA>

A:Cross-references: GB:U13660; NID:g600731; PID:g600732

C:Genetics:

A:Gene: GDB:CDMP1

A:Cross-references: GDB:438940

C:Superfamily: inhibin

Query Match 43.4%; Score 762; DB 2; Length 501;
Best Local Similarity 50.6%; Pred. No. 7.6e-50;
Matches 164; Conservative 46; Mismatches 64; Indels 50; Gaps 11;

Qy 9 LRRQKYLFDVSMDSKDELVAELRLFRQAPSAPWGPAGP-----LHVQLFPCLSL--- 59
Db 217 VRKQRYVFDISAL-EKDGLLGAELRLRKKPS-DTAKPAVPRSRRAAQLKLSSCPSGRQ 274
Qy 60 PLLDARTLDPQAGPAGWEVDVWQGLRH-OPWKQLCLLELAANGELDAGEAEARAGP 118
Db 275 ALLDVRSV--PGLDGSWEVDFINKLFRNFKNSAQLCLEL-----FAEMRGR-- 320
Qy 119 QPPPPDLRLSGFGRVRPPQERALLVFTSRQKNL-FAEMREOLGSAEAGPGAGAE 177
Db 321 ---TVDLRGLGFDRAARQVHEKALFLVFGTRKKRDLFFNEIKARSGQDDKT----- 368
Qy 178 SWPPPGAPDARPLSPGRRRRRTAFASRHGKRRHKKSLRCSKKPLHVNFKELGWDDW 237
Db 369 -----VVEYLFSQ--RRKRRAPLATROGKRPSKRLKARCSRKALHVNFKDGMGDDW 417
Qy 238 IAPLEYEAYHCEGVCDFFPLRSHLEPTNHAIQTLMNSMDPGSTPPSCCVPTKLTPISI 297
Db 418 IAPLEYEAFHCEGLCEFPPLRSHLEPTNHAVIOTLMNSMDPESTPTCCVPTRLSPISI 477
Qy 298 YIDAGNNVYKQYEDMVVESCGR 321
Db 478 FIDSANNVYKQYEDMVVESCGR 501

RESULT 5

S43295

bone morphogenetic protein homolog GDF6 precursor - mouse (fragment)
 M:Alternate names: growth and differentiation factor 6
 C:Species: Mus musculus (house mouse)
 C:Date: 20-Oct-1994 #sequence_revision 07-Feb-1997 #text_change 26-May-2000
 C:Accession: S43295
 R:Storm, E.E.; Huynh, T.V.; Copeland, N.G.; Jenkins, N.A.; Kingsley, D.M.; Lee, S.J.
 Nature 368, 639-643, 1994
 A:Title: Limb alterations in brachypodism mice due to mutations in a new member of the FGF-1-5 domain: polybasic protease recognition site #status predicted <PPR>
 A:Reference number: S43294; MUID:94195427
 A:Accession: S43295
 A:Molecule type: DNA
 A:Residues: 1-125 <STO>
 A:Cross-references: EMBL:U08338; NID:9488463; PIDN:AAA18779.1; PID:9488464
 C:Genetics:
 A:Gene: gdf6
 C:Superfamily: inhibin
 F:1-5/Domain: polybasic protease recognition site #status predicted <PPR>
 F:6-125/Product: bone morphogenetic protein homolog GDF6 (fragment) #status predicted <M

Query Match 39.3%; Score 691; DB 2; Length 125;
 Best Local Similarity 99.2%; Pred. No. 4.1e-45;
 Matches 124; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 197 RRRRTAPASRHGKRRKSKRLRCKKPLHVNFKELGWDWIIAPLEYAYHCEGVCDPP 256
 |||||
 Db 1 RRRRTAPASRHGKRRKSKRLRCKKPLHVNFKELGWDWIIAPLEYAYHCEGVCDPP 60
 |||||

QY 257 LRSLEPTTHAIQTLLNSMDPGSTPPSCVPTKLTPISTILYIDAGNNVVKQYEDMVVE 316
 |||||
 Db 61 LRSLEPTTHAIQTLLNSMDPGSTPPSCVPTKLTPISTILYIDAGNNVVKQYEDMVVE 120
 |||||

QY 317 SCGR 321
 |||||

Db 121 SCGR 125

RESULT 6

S43296
 bone morphogenetic protein-related protein (GDF7) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 19-May-2000
 C:Accession: S43296
 R:Storm, E.E.; Huynh, T.V.; Copeland, N.G.; Jenkins, N.A.; Kingsley, D.M.; Lee, S.J.
 Nature 368, 639-643, 1994
 A:Title: Limb alterations in brachypodism mice due to mutations in a new member of the FGF-1-5 domain: polybasic protease recognition site #status predicted <PPR>
 A:Reference number: S43294; MUID:94195427
 A:Accession: S43296
 A:Molecule type: DNA
 A:Residues: 1-151 <STO>
 A:Cross-references: GB:U08339; NID:9488465; PIDN:AAA18780.1; PID:9488466
 C:Superfamily: inhibin

Query Match 31.2%; Score 549; DB 2; Length 151;
 Best Local Similarity 59.5%; Pred. No. 2.3e-34;
 Matches 103; Conservative 13; Mismatches 35; Indels 22; Gaps 1;

QY 149 RSQRKNLFPNREQLGSAEAGPAGAGAGSWPPPGAPDARPLWPSGRRRRRTAFASRH 208
 |||||
 Db 1 RRRRTALACTGAQSGGGGGGGGGGGGGGGG----- 38

QY 209 KRRGKSKLRCKSKKPLHVNFKELGWDWIIAPLEYAYHCEGVCDFFPLRSHLEPTNHAI 268
 |||||
 Db 39 GRGHRGRCRCKSKRLHVDKELGWDWIIAPLDYAYHCEGVCDFFPLRSHLEPTNHAI 98
 |||||

QY 269 IOTLLNSMDPGSTPPSCVPTKLTPISTILYIDAGNNVVKQYEDMVVEGCGR 321
 |||||

Db 99 IOTLLNSMDPGSTPPSCVPTKLTPISTILYIDAGNNVVKQYEDMVVEGCGR 151
 |||||

RESULT 7

JH0688
 bone morphogenetic protein 2II precursor - African clawed frog
 C:Species: Xenopus laevis (African clawed frog)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999
 C:Accession: JH0688
 R:Nishimatsu, S.; Suzuki, A.; Shoda, A.; Murakami, K.; Ueno, N.
 Biochem. Biophys. Res. Commun. 186, 1487-1495, 1992
 A:Title: Genes for bone morphogenetic proteins are differentially transcribed in ear
 A:Reference number: JH0687; MUID:92378616
 A:Accession: JH0688
 A:Molecule type: mRNA
 A:Residues: 1-398 <NIS>
 A:Cross-references: GB:X63425; NID:964583; PIDN:CAA45019.1; PID:964584
 A:Experimental source: oocyte
 C:Superfamily: inhibin
 C:Keywords: glycoprotein
 F:285-398/Product: bone morphogenetic protein 2II #status predicted <MAT>
 F:137,202,237,340/Binding site: carbonyl site: Asn (covalent) #status predicted

Query Match 24.3%; Score 426.5; DB 2; Length 398;
 Best Local Similarity 31.3%; Pred. No. 9.7e-25;
 Matches 104; Conservative 51; Mismatches 90; Indels 87; Gaps 12;

QY 12 QKYLEFDVSMLSKDELVGAEELRFRQAPSAPWGPAGPLH-VQLPCLSLP----- 61
 |||||
 Db 132 QRFENLSSIPDEELVTSELRIREFQVOEPKTDGSKLHRIINIDYIVKPAASRGPPV 191
 |||||

QY 62 -LLDARTLDPOCAPAGWEVFDVWQGL-----RHQPWKQCLCELRANGELDAGAEARA 115
 |||||

Db 192 RLDDTLRIHNN--ESKWESEFDVTPAIRTWIAHKQPNHGFVEVTHLNDNTNPKRHVRI 248
 |||||

QY 116 RGPQPPPPDLRLS-----GFGRRVRPPQRRALLYVFTTSQRKNLFAEMREQLGSAEAGP 171
 |||||

Db 249 S-----RSLTDKGHWPRIRP-----LLVTFSHD-----GK 274

QY 172 GAGAGSGPPPPSGAPDARPLWPSGRRRRRTAFASRRHGRKGRKSLR--CSKKPLHVN 229
 |||||

Db 275 GHALH-----KQKQQA-----RHQKRLKSSCRHPLLYVDF 307

QY 230 KELGWDWIIAPLEYAYHCEGVCDFFPLRSHLEPTNHAIQTLLNSMDPGSTPPSCVPT 289
 |||||

Db 308 SDVGWMDWIVAPPGYHAFYCHCEGFPPLADHLNSTHAIQVTLVNSVT-NIPKACCVPT 366
 |||||

QY 290 KLTPTISILYIDAGNNVVKQYEDMVVEGCGR 321
 |||||

Db 367 ELSATSMILYLDENKXVVLKNYQDMVVEGCGR 398
 |||||

RESULT 8

JH0687
 bone morphogenetic protein 2I precursor - African clawed frog
 C:Species: Xenopus laevis (African clawed frog)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999
 C:Accession: JH0687; S16244
 R:Nishimatsu, S.; Suzuki, A.; Shoda, A.; Murakami, K.; Ueno, N.
 Biochem. Biophys. Res. Commun. 186, 1487-1495, 1992
 A:Title: Genes for bone morphogenetic proteins are differentially transcribed in ear
 A:Reference number: JH0687; MUID:92378616
 A:Accession: JH0687
 A:Molecule type: mRNA
 A:Residues: 1-398 <NIS>
 A:Cross-references: GB:X63424; NID:964585; PIDN:CAA45018.1; PID:964586
 A:Experimental source: oocyte
 R:Plessow, S.; Koester, M.; Knoechel, W.
 Biochim. Biophys. Acta 1089, 280-282, 1991
 A:Title: cDNA sequence of Xenopus laevis bone morphogenetic protein 2 (BMP-2).
 A:Reference number: S16244; MUID:91274367
 A:Accession: S16244
 A:Molecule type: mRNA
 A:Residues: 1-6,'S',8-15,'V',17-232,'N',234-398 <PLE>
 A:Cross-references: EMBL:X55031; NID:964581; PIDN:CAA38850.1; PID:964582

C:Superfamily: inhibin
C:Keywords: dimer; glycoprotein
F:285-398/Product: bone morphogenetic protein 21 #status predicted <MAT>
F:137,202,340/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 24.2%; Score 425.5; DB 2; Length 398;
Best Local Similarity 31.8%; Pred. No. 1.1e-24;
Matches 105; Conservative 51; Mismatches 88; Indels 89; Gaps 13;

QY 12 QKYLFDVSMLSKDEELVGAELRFRQAPSPAGPLH-VOLFPCLSLP----- 61
DB 132 ORFFNLSSIPNEELVTSAEIRFREQVQPFSDSKLHRIINIDIVKPAASARCPVV 191
QY 62 -LLDARTLDPOGAPPAGNEVDVWQGL-----RHQPWKQLCLELRAAWGELDAGEAEARA 115
DB 192 RLDDTRLVHHN---ESKWESFDVTPAIAIAHQPHGFWVEVT-----HLD----- 236
QY 116 RGPQPPPPDLRLSLGFGRRVRP-----POERALLVVFTRSORKNLFAEMREQLGSAAAG 170
QY 237 -NDRNVFKHVR---ISRLTPDKDNWQPIRLVLVTFSDH-----G 273
QY 171 PGAGAEGSWPPPGADARPWLPSPGRRRTAFASRHGKRGKKSRLR--CSKKPLHVN 228
DB 274 KGHALH-----KQKQQA-----RHKQRKLSKSCRRHPLVYD 306
QY 229 FKELGWDWIIAPLEYAYHCEGVCDFPLRSHLEPTNHAIQTLMNSMDPGSTPPSCCV 288
DB 307 FSDVGMNDWIVAPPGYHAFYCHGECPEPLADHLNSTHAIQTLVNSVNT-NIPKACV 365
QY 289 TKLTPISILYIDAGNNVYKQYEDMVVESCGR 321
DB 366 TELSAILMLYDENKVVLYNQMVEGCGCR 398

RESULT 9
I50608
bone morphogenetic protein 4 - chicken
C:Species: Gallus gallus (chicken)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999
C:Accession: I50608
R:Francis, P.H.; Richardson, M.K.; Brickell, P.M.; Tickle, C.
Development 120, 209-218, 1994
A:Title: Bone morphogenetic proteins and a signalling pathway that controls patterning
A:Reference number: I50607; MUID:94163974
A:Accession: I50608.
-A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
Residues: 1-405 <PRA>
Cross-references: EMBL:X75915; NID:g472929; PIDN:CAA53514.1; PID:g472930
Genetics:
A:Gene: Bmp-4
C:Superfamily: inhibin

Query Match 23.8%; Score 418.5; DB 2; Length 405;
Best Local Similarity 31.8%; Pred. No. 3.9e-24;
Matches 104; Conservative 47; Mismatches 101; Indels 75; Gaps 11;

QY 11 RQKYLFDVSMLSKDEELVGAELRFR---QAPSAPWGPAGPLHVQLFPCLSLP----- 61
DB 138 RIRFVNLSVPDNEVSSLELRLRYRQVEPSANW---ERGFHINITYEVKPKLRSQA 195
QY 62 ---LLDARTLDPOGAPPAGNEVDVWQGLRHQPWKQLCLELRAAWGELDAGEAEARANGP 118
DB 196 ITRLLDTRLVHHN---VTRWETFDV-----SPAVIRWTKD 227
QY 119 QPPPPDLRLSLGFGRRVRPQERALLVVFTRSORKNLFAEMREQLGSAAAGPGAGAGS 178
DB 228 KQP-----NHLGVIEVTHLHQATHQCKHVRIRSLPQGHG-----GD 265
QY 179 WPPPSGADARPWLPS---PGRRRRTAFASRHGKRGH-KKSRLRCSKKPLHVNFKELGW 234

DB 266 W-----AQLRPLLVTFGHDGRGHALTTRRRSPKHGSRKKNKRRHRLHYVDFSDVGW 319
QY 235 DWIITAPLEYAYHCEGVCDFPLRSHLEPTNHAIQTLMNSMDPGSTPPSCCVTKLTPI 294
DB 320 NDWIVAPPGYQAFYCHGDCPFPLADHLNSTHAIQTLVNSVN-SSIPKACCVPELSAI 378
QY 295 SILYIDAGNNVYKQYEDMVVESCGR 321
DB 379 SMLYLDYDKVVLKKNYQEMVVEGCGCR 405

RESULT 10
BMH04
bone morphogenetic protein 4 precursor - human
N:Alternate names: bone morphogenetic protein 2B
C:Species: Homo sapiens (man)
C:Date: 16-Sep-1992 #sequence_revision 03-Aug-1995 #text_change 18-Jun-1999
C:Accession: C37278
R:Wozney, J.M.; Rosen, V.; Celeste, A.J.; Mitsock, L.M.; Whitters, M.J.; Kriz, R.W.;
Science 242, 1528-1534, 1988
A:Title: Novel regulators of bone formation: molecular clones and activities.
A:Reference number: A37278; MUID:89072730
A:Accession: C37278
A:Molecule type: mRNA
A:Residues: 1-408 <W03>
A:Cross-references: GB:M22490; NID:g179503; PIDN:AAA51835.1; PID:g179504
C:Genetics:
A:Gene: GDB:BMP4; BMP2B
A:Cross-references: GDB:125205; OMIM:112262
A:Map position: 14q22-14q23
C:Superfamily: inhibin
C:Keywords: bone; glycoprotein
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-292/Domain: propeptide #status predicted <PRO>
F:293-408/Product: bone morphogenetic protein 4 #status predicted <MAT>
F:143,208,350,365/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 23.1%; Score 406.5; DB 1; Length 408;
Best Local Similarity 31.7%; Pred. No. 3.2e-23;
Matches 106; Conservative 43; Mismatches 96; Indels 89; Gaps 11;

QY 13 KYLFDVSMLSKDEELVGAELRFR---QAPSAPWGPAGPLHVQLFPCLSLP----- 55
DB 139 RFLFNLSIPDNEVSSLELRLFRQVDPGDPWGRGFRHINITYEVKPKPAEVVPGH---- 194
QY 56 PCLSPILLDARTLDPOGAPPAGNEVDVWQGLRHQPWKQLCLELRAAWGELDAGEAEARA 115
DB 195 -LITRLDTRLVHHN---VTRWETFDV----- 217
QY 116 RGPQPPPPDLRLSLGFGRRVRPQERALLVVFTRSORKNLFAEMREQLGSAAAGPGAGA 175
DB 218 -----SPAVLR---WTRKQPNYGLAIEVTHLHQTRTHQGHVIRISLSPQGS----- 262
QY 176 EGSWPPSPGADARPWLPSGR-----RRRTAFASRHGKRGKKSRLRCSKKPLHV 227
DB 263 -GNW-----AQLRPLLVTFGHDGRGHALTTRRRSPKHGSRKKNKRRHRLHYV 315
QY 228 NFKELGWDWIIAPLEYAYHCEGVCDFPLRSHLEPTNHAIQTLMNSMDPGSTPPSCCV 287
DB 316 DESDVGNDWIVAPPGYQAFYCHGDCPFPLADHLNSTHAIQTLVNSVN-SSIPKACCV 374
QY 288 PKLTPISILYIDAGNNVYKQYEDMVVESCGR 321
DB 375 PTELSAISMLYLDYDKVVLKKNYQEMVVEGCGCR 408

RESULT 11
I49542
bone morphogenetic protein 5 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Jul-1999
C:Accession: I49542

R:King, J.A.; Marker, P.C.; Seung, K.J.; Kingsley, D.M.

Dev. Biol. 166, 112-122, 1994
A:Title: BMP5 and the molecular, skeletal, and soft-tissue alterations in short ear mice
A:Reference number: I49542; MUID:95046894

C:Accession: I49542

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-452 <RES>

A:Cross-references: GB:L41145; NID:g755033; PIDN:AAA64612.1; PID:g755034

C:Genetics:

A:Gene: BMP5

C:Superfamily: inhibin

Query Match 23.1%; Score 405.5; DB 2; Length 452;

Best Local Similarity 29.0%; Pred. No. 4.2e-23;

Matches 96; Conservative 54; Mismatches 126; Indels 55; Gaps 8;

QY 1 NSDLSHTPLRRKOKYLFVDVSMLSKDEELVCAELRFRQAPSAPWGPAGPLHVLFPCLSP 60

165 DDFSHORHYKEFEDLTOIPHGAIVAAEFRIYKDKGNIRFENET--IKISYQIIKE 222

QY 61 -----LLDARTLDPOGAPPAGWVDFVWQGLRH---QPKWLCLLELRAAMGELDAG 109

223 YTNRDADFLDLTRKTQ---ALDVGWLVFDITVTSNHWVINPQNNLGLQLCAETGD---G 276

QY 110 EAEARAGPQQPPDLRLSLGRRVRPQERALLVYTRSORKNLFAEMREQLGSABAA 169

DL 277 RS-----INVKSAGLVGRHQPSQKPPFMAVFKAEE-----VLLRSVRAAARKK 320

QY 170 GPCGAGEGSWPPSGAPDAPRWLPSPGRRRRRTAFASRHGRHKKSLRCSKKPLHWNF 229

Db 321 NQNRKNSHQDPSPMPA-----GDYNTSEQKQACKKHLYVSF 360

QY 230 KELGWDDWIIAPLEYAHCYGVCDPFLRSHLEPTNHAIIQTLNMSMDPSTPPSCCVPT 289

Db 361 RDLGWDDWIIAPLEYAHCYGVCDPFLRSHLEPTNHAIIQTLNMSMDPSTPPSCCVPT 420

QY 290 KLTPISILYIDAGNNVYKQYEDMVVESC GC 320

Db 421 KLNALSVLYFDSSNVILKKYNNVVRSCGC 451

RESULT 12

S52408

SPDVR1 protein - sea urchin (Strongylocentrotus purpuratus)

C:Species: Strongylocentrotus purpuratus (purple urchin)

A:Reference number: S52408

A:Accession: S52408

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-461 <PONS>

A:Cross-references: EMBL:Z48313; NID:9673496; PID:9673497

C:Superfamily: inhibin

Query Match 23.1%; Score 405.5; DB 2; Length 461;

Best Local Similarity 32.4%; Pred. No. 4.2e-23;

Matches 108; Conservative 42; Mismatches 104; Indels 79; Gaps 12;

QY 13 KYLFVDSMLSDEELVCAELRFRQAPSAPWGPAGPLHVLFPCLSP 66

Db 182 RYFEDIGRIPOGETVTSALRVRDA--GROGRSLYRIDVLLRERSGDSRSPYLDST 239

QY 67 TLDPOGAPPAGWVDFV-----WGLRHQPKWLCLLELRAAMGELDAGEAPARAGPQQ 120

Db 240 IV---CAGDHGWLVDMTSATSTW---RSYPCANVGLQLRVE--SLQGLNID----- 283

QY 121 PPPDLRLSLGFRVRPQERALLVYTRSQ-----RKNLFAEMREQLGSAAAGP 171

Db 284 --PTDAGVVGNGN--NEGREFPMVVFQNEEVYATNHLRRNRRAATROKKG----- 332

QY 172 GAGAGSWPPSPGAPDAPRWLPSPGRRRR---TAFASRHGRHKKSLRCSKKPLHV 227

Db 333 -----GKRPRKPTDNDIASR--DSASSLNSDWQCKRKNLFV 367

QY 228 NFKELGWDDWIIAPLEYAHCYGVCDPFLRSHLEPTNHAIIQTLNMSMDPSTPPSCCV 287

Db 368 NFKELGWDDWIIAPLEYAHCYGVCDPFLRSHLEPTNHAIIQTLNMSMDPSTPPSCCV 427

QY 288 PTKLTPISILYIDAGNNVYKQYEDMVVESC GC 320

Db 428 PTKLTPISILYIDAGNNVYKQYEDMVVESC GC 460

RESULT 13

S37073

bone morphogenetic protein 2 - rat

C:Species: Rattus norvegicus (Norway rat)

A:Reference number: S37073

A:Accession: S37073

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-393 <PENS>

A:Cross-references: EMBL:Z25868; NID:g397950; PIDN:CAA81088.1; PID:g397951

C:Superfamily: inhibin

Query Match 22.8%; Score 401; DB 2; Length 393;

Best Local Similarity 30.8%; Pred. No. 7.9e-23;

Matches 105; Conservative 50; Mismatches 98; Indels 88; Gaps 13;

QY 2 SLSHTPLRRKOKYLFVDVSMLSKDEELVCAELRFRQAPSAPWGPAGPLHVLFPCLSP 61

Db 120 SEMSGKTSRR--FFENLSSVPTDEFLTSAELQIFREQMQLGNSFOHRIYIETKPA 177

QY 62 -----LLDARTLDPOGAPPAGWVDFVWQGLRHQPKWLCLLELRAAMGELDAGEA 111

Db 178 TASSKFPVTRLDLRLVTQN---TSQWESFVDTFAYVR--W-----TAQHTNHGFV 224

QY 112 EARGPQQPPPPDLRLSLGFRVRPQERALLVYTRSORKNLFAEMREQLGSAAAGP 171

Db 225 VEVAHLEKP-----GVSKR-----HVRISRLHOD----- 250

QY 172 GAGAGSWPPSPGAPDAPRWLPSPG-----RRRRTAFASRHGRHKKSLRLR--C 220

Db 251 ----EHSW-----SQVRPLLVTFEGHCKGHPKHKREKQA-----KKQKRLKSSC 293

QY 221 SKKPLHVNFKELGWDDWIIAPLEYAHCYGVCDPFLRSHLEPTNHAIIQTLNMSMDP 280

Db 294 KRHLVYDFSDVGNWDMIVAPPGTHAFYCHGCEFPPLADHLNLTNHAIVQLVNSVN-SK 352

QY 281 TPPSCCVPTKLTPISILYIDAGNNVYKQYEDMVVESC GC 321

Db 353 IPKACCVPTLSALSMYLDENKVKVNLKYNQDMVVEGCGC 393

RESULT 14

I49541

bone morphogenetic protein 4 - mouse

C:Species: Mus musculus (house mouse)

A:Reference number: S29523; B34201

A:Accession: I49541; S29523; B34201

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-461 <PONS>

A:Cross-references: EMBL:Z28373, 1995

C:Superfamily: inhibin

Query Match 23.1%; Score 405.5; DB 2; Length 461;

Best Local Similarity 32.4%; Pred. No. 4.2e-23;

Matches 108; Conservative 42; Mismatches 104; Indels 79; Gaps 12;

QY 13 KYLFVDSMLSDEELVCAELRFRQAPSAPWGPAGPLHVLFPCLSP 66

Db 182 RYFEDIGRIPOGETVTSALRVRDA--GROGRSLYRIDVLLRERSGDSRSPYLDST 239

QY 67 TLDPOGAPPAGWVDFV-----WGLRHQPKWLCLLELRAAMGELDAGEAPARAGPQQ 120

Db 240 IV---CAGDHGWLVDMTSATSTW---RSYPCANVGLQLRVE--SLQGLNID----- 283

Query Match	22.6%	Score	396.5;	DB	1;	Length	454;
Best Local Similarity	28.8%;	Pred.	No. 2e-22;				
Matches	98;	Conservative	51;	Mismatches	118;	Indels	73;
Caps	9;						
Qy	1	NSDSLHTPLRRKQYLFVDSMLSDEELVGAEFLRFOAPSAPGPPAGLHVOLFPCCLSP	60	:	:	:	:
Db	167	DKDFSHORRYHYKERFOLTOIPHGEAVTAAEFRYYKDRSNRNRENET--IKISIYQIKE	224	:	:	:	:
Qy	61	-----LLLDARTLPQGAPGAPGAVEGVFWMOGLRH--QPWKQLCLELRAAWGLDAG	109	:	:	:	:
Db	225	YTNRADLFLDLTRKAQ---ALDVGLWFVDITYTSNHWVINPQNNLGLQLCAETGD---G	278	:	:	:	:
Qy	110	EAEARAGPOQQPPDDLRSLGFRGRVRPPGERALLVVVTRSQRKNLFAENREQLSGAEA	169	:	:	:	:
Db	279	RS-----INVKSAGLVGRQGPQSQKQPMVAF-----FKASEVLRLSRVAA	318	:	:	:	:
Qy	170	GPGAGAGSPPPSPGADARPWLPSGPRRRRTTAFASRH-----GKRHGKKSLRC	220	:	:	:	:
Db	319	NK-----RKWNRRNKSSHQDSSSMSSVGYNTSEQKOAC	353	:	:	:	:
Qy	221	SKPLHVNFKELGWDDWIITAPLEYEAYHCBCVCDFPLURSHLEPTNHAIIOITLMNSMDPGS	280	:	:	:	:
Db	354	KKHELYVSFDRLGHQDWIIAPEGYAAPCYDGESFPNLNAHMNATNHAIVOTLVHLMPDH	413	:	:	:	:
Qy	281	TPSCCVPTKLTPISILYIDAGNNVYKYQYEDMVVESCGC	320	:	:	:	:
Db	414	VPKPCCATKLNAISLYFYDFSNNVILUKYRNVMVVRSGC	453	:	:	:	:

Search completed: October 3, 2002, 15:39:45
Job time: 181 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 3, 2002, 15:45:59 ; Search time 17.39 Seconds
(without alignments)
714.720 Million cell updates/sec

Title: US-09-945-182-26

Perfect score: 1757

Sequence: 1 NSDLSTPLRQKYLFDVSM.....GNVVYKQYEDMVVSCCR 321

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

al number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1368	77.9	436	1	GDF6_BOVIN
2	771	43.9	501	1	GDF5_HUMAN
3	765	43.5	495	1	GDF5_MOUSE
4	691	39.3	125	1	GDF6_MOUSE
5	549	31.2	151	1	GDF7_MOUSE
6	426.5	24.3	338	1	BMP4_XENLA
7	426.5	24.3	398	1	BMP4_XENLA
8	418.5	23.8	405	1	BMP4_CHICK
9	406.5	23.1	408	1	BMP4_HUMAN
10	405.5	23.1	452	1	BMP5_MOUSE
11	405.5	23.1	461	1	DVRL_STRPU
12	403.5	23.0	395	1	BMP2_RABIT
13	401	22.8	393	1	BMP2_RAT
14	401	22.8	408	1	BMP4_MOUSE
15	398.5	22.7	409	1	BMP4_RABIT
16	396.5	22.6	454	1	BMP5_HUMAN
17	396	22.5	408	1	BMP4_RAT
18	395	22.5	394	1	BMP2_MOUSE
19	392.5	22.3	396	1	BMP2_DAMDA
20	388.5	22.1	396	1	BMP2_HUMAN
21	386	22.0	430	1	BMP7_MOUSE
22	386	22.0	431	1	BMP7_HUMAN
23	385.5	21.9	402	1	BMP8_HUMAN
24	384	21.9	426	1	BMP7_XENLA
25	382.5	21.8	399	1	BMP4_MOUSE
26	380	21.6	424	1	BMP10_HUMAN
27	378	21.5	408	1	BMP4_DAMDA
28	377	21.5	401	1	BMP4_XENLA
29	375	21.3	333	1	BMP2_CHICK
30	372	21.2	420	1	BMP10_MOUSE
31	371.5	21.1	621	1	DECA_DROPS
32	369	21.0	588	1	DECA_DROME
33	369	21.0	593	1	DECA_DROSI

34	362.5	20.6	354	1	NODA_MOUSE	P43021	mus musculus
35	362.5	20.6	395	1	UNIV_STRPU	P48970	strongyloce
36	362.5	20.6	428	1	GDF2_MOUSE	Q9W556	mus musculus
37	360	20.5	510	1	BMP6_MOUSE	P20722	mus musculus
38	356.5	20.3	429	1	GDF2_HUMAN	Q9UK05	homo sapien
39	353	20.1	372	1	DECA_TRICA	Q26974	tribolium c
40	351	20.0	513	1	BMP6_HUMAN	P22004	homo sapien
41	344.5	19.6	355	1	DVRL_BRARE	P35621	brachydanio
42	339.5	19.3	427	1	DSLI_CHICK	P34822	gallus gall
43	334	19.0	207	1	BMP6_RAT	Q04906	rattus norv
44	332	18.9	455	1	60A_DROME	P27091	drosophila
45	331.5	18.9	399	1	BM8B_MOUSE	P55105	mus musculus

ALIGNMENTS

RESULT	1
GDF6_BOVIN	
ID	GDF6_BOVIN
AC	P55106;
DT	01-OCT-1996 (Rel. 34, Created)
DT	01-OCT-1996 (Rel. 34, Last sequence update)
DT	16-OCT-2001 (Rel. 40, Last annotation update)
DE	Growth/differentiation factor 6 precursor (GDF-6) (Cartilage-derived morphogenetic protein 2) (CDMP-2) (Fragment).
DE	GDF6 OR CDMP2.
GN	Bos taurus (Bovine).
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC	Bovidae; Bovinae; Bos.
OX	NCBI_TaxID=9913;
OX	[1]
RP	SEQUENCE FROM N.A.
RX	TISSUE=Articular cartilage;
RX	MEDLINE=95050604; PubMed=7961761;
RA	Chang S., Hoang B., Thomas J.T., Vukicevic S., Luyten F.P., Ryba N.J.P., Kozak C.A., Reddi A.H., Moos M.;
RT	*Cartilage-derived morphogenetic proteins. New members of the transforming growth factor-beta superfamily predominantly expressed in long bones during human embryonic development.*;
RT	J. Biol. Chem. 269:28227-28234(1994).
RL	- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC	- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC	-----
CC	EMBL; U13661; AAA61416.1; -
DR	HSSP; P18075; 1BMP.
DR	InterPro: IPR001839; TGF-beta.
DR	InterPro: IPR001111; TGFb.N.
DR	Pfam; PF00019; TGF-beta; 1.
DR	Pfam; PF00688; TGFb_propeptide; 1.
DR	ProDom; PD000357; TGF-beta; 1.
DR	SMART; SM00204; TGFb; 1.
DR	PROSITE; PS00250; TGF_BETA.1; 1.
KW	Growth factor; Cytokine; Glycoprotein.
FT	NON_TER
FT	PROPEP
FT	CHAIN
FT	DISULFID
FT	DISULFID
FT	DISULFID
FT	DISULFID
FT	CARBOHYD
FT	SEQUENCE

Query Match 77.9%; Score 1368; DB 1; Length 436;
Best Local Similarity 81.7%; Pred. No. 8.6e-93;
Matches 268; Conservative 9; Mismatches 39; Indels 12; Gaps 6;

QY 3 DLSTPLRRKQYLFVDSMLSKELVGAELRLFRQAPSPAPGPPACPLHVLQVLPCLSPILL 62
DB 112 DLSTPLRRKQYLFVDSMLSKELVGAELRLFRQAPALAPPAALPLAALRLP-VAPAA 170
QY 63 LDARTLDPOCAPAGVEFVDMGLRHQPKWQKLCLELRAAW-GELDAGAEARARAPQOP 121
DB 171 GSAEP-CPACAPRGVEFVDMGLRHQPKWQKLCLELRAAWGEGPAAEDARTPQOP 229
QY 122 PPDLSRLSGRRVPPQERALLVTRSORKNLFEMREQLGSA-EAAGPGAGAGSGW- 179
DB 230 PPDLSRLSGRRVPPQERALLVTRSORKNLFEMREQLGSAEYVVGPGGAGSGP 289
QY 180 -----PPPSGAPDARPLPSPGRRRRRTAFASRHCKRHKSLRCLSCKPLHVNFKELG 233
DB 290 PPDPPPPPPSGTDPAGLWSPSG-RRRTAFASRHCKRHKSLRCLSCKPLHVNFKELG 348
QY 234 WDDWIIAPLEYAYHCEGVCDFPLRSHLEPTNHAIQTLMNSMDPGSTPPSCCVPTKLT 293
DB 349 WDDWIIAPLEYAYHCEGVCDFPLRSHLEPTNHAIQTLMNSMDPGSTPPSCCVPTKLT 408
QY 294 ISILYIDAGNNVYKQYEDWVWESGCR 321
DB 409 ISILYIDAGNNVYNEEYVWVWESGCR 436

RESULT 2
GDF5_HUMAN STANDARD; PRT; 501 AA.

AC P43026; Q96SBI;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Growth/differentiation factor 5 precursor (GDF-5) (Cartilage-derived morphogenetic protein 1) (CDMP-1).
DE GDF5 OR CDMP1.
GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
Y MEDLINE=95071375; PubMed=7980526;
Hootten G., Neidhardt H., Jacobowsky B., Pohl J.;
"Cloning and expression of recombinant human growth/differentiation factor 5";
RL Biochem. Biophys. Res. Commun. 204:646-652(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Articular cartilage;
RX MEDLINE=95050604; PubMed=7961761;
RA Chang S., Hoang B., Thomas J.T., Vukicevic S., Luyten F.P.,
RYba N.J.P., Kozak C.A., Reddi A.H., Moos M.;
"Cartilage-derived morphogenetic proteins. New members of the transforming growth factor-beta superfamily predominantly expressed in long bones during human embryonic development.";
RL J. Biol. Chem. 269:28227-28234 (1994).
RN [3]
RP SEQUENCE FROM N.A.
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baggeley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Copley V.E., Collier R.E., Connor R., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhani P., Dunn M.,

Query Match

43.9%; Score 771; DB 1; Length 501;

RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Graham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Levasalho M.H., Leversha M., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McNurray A.A.,
RA Milne S., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkhen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whittaker S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
Rogers J.;
"The DNA sequence and comparative analysis of human chromosome 20";
Nature 414:865-871(2001).
CC -!- FUNCTION: COULD BE INVOLVED IN BONE FORMATION.
CC -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC -!- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN LONG BONES DURING HUMAN EMBRYONIC DEVELOPMENT.
CC -!- DISEASE: DEFECTS IN GDF5 ARE A CAUSE OF ACROMESOMELIC CHONDRODYSPLASIA OF THE HUNTER-THOMPSON TYPE. THIS FORM OF DWARFISM IS CHARACTERIZED BY SHORT FOREARMS, HANDS AND FEET. THE RADIUS IS CURVED AND ITS HEAD IS OFTEN DISLOCATED POSTERIORLY. THE METACARPALS, METATARSALS AND PHALANXES ARE PARTICULARLY SHORT. THE PHALANXES ARE ALMOST SQUARE.
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
EMBL; X80915; CAA56874.1; -;
DR EMBL; U13660; AAA57007.1; -;
DR EMBL; AL121586; CAB89416.1; -;
DR HSSP; PL2643; 3BMP.
DR MIM; 601146; -;
DR MIM; 201250; -;
DR MIM; 200700; -;
DR InterPro; IPR002400; GF_cysknot.
DR InterPro; IPR001839; TGF-beta.
DR InterPro; IPR001111; TGFb.N.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR ProDom; PD000357; TGF-beta; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Signal; Growth factor; Cytokine; Glycoprotein.
FT SIGNAL 1 27 POTENTIAL.
FT PROPEP 28 381 POTENTIAL.
FT CHAIN 382 501 GROWTH/DIFFERENTIATION FACTOR 5.
FT DISULFID 400 466 BY SIMILARITY.
FT DISULFID 429 498 BY SIMILARITY.
FT DISULFID 433 500 BY SIMILARITY.
FT DISULFID 465 465 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 189 189 N-LINKED (GLCNAC...) (POTENTIAL).
FT CONFLICT 38 38 T -> S (IN REF. 2).
FT CONFLICT 254 258 APGGG -> VPSR (IN REF. 2).
FT CONFLICT 276 276 S -> A (IN REF. 2).
FT CONFLICT 321 321 A -> T (IN REF. 2).
FT CONFLICT 384 384 L -> S (IN REF. 2).
SQ SEQUENCE 501 AA; 55410 MW; 37985F2D15C4F5EF CRC64;

```

DR PRINTS: PR00438; GFCYSKNOT.
DR ProDom: PD000357; TGF-beta; 1.
DR SMART: SM00204; TGF-beta; 1.
DR PROSITE: PS00250; TGF-BETA_1; 1.
DR KW Signal: Growth factor; Cytokine; Glycoprotein; Polymorphism.
FT SIGNAL 1 27
FT PROPEP 28 375
FT CHAIN 376 495
FT DISULFID 394 460
FT DISULFID 423 492
FT DISULFID 427 494
FT DISULFID 459 459
FT CARBOHYD 183 183
FT VARIANT 98 98
FS SEQUENCE 495 AA; 54885 MW; CDDSDSE48185D2E3 CRC64;

Query Match 43.5%; Score 765; DB 1; Length 495;
Best Local Similarity 50.5%; Pred. No. 7.9e-49;
Matches 163; Conservative 50; Mismatches 62; Indels 48; Gaps 12;

Qy 9 LRRQKLYDFVSNLSDKEELVGAELRLFRQAP---SAPWGPPAGPL-HVOLFPCLSL----P 60
Db 211 VRKQYVFDISAL-EKDGLLGAELRLRKPLDVAKPVPSSGRVQAQLKLSGPCSGROPA 269

Qy 61 LLDAITLDPGAPAGAGHEVEDVWGLRH-OPWKOLCLLELRANGELDAGAEARARGPQ 119
Db 270 ALLDVRVS--PGLDGSQGEVFDIWKLFNFKNQAQLCLEL-AM---ERGRA----- 315

Qy 120 QPPPLRLSLRGRRVRPPQERALLVWTRSRKNL-FAEMREQLGSAEAAAGPGAGEGS 178
Db 316 ----VDLRGLGFERTARQVHEKALFLVFGRTKKRDLFFNEIKARSGQDDKT----- 362

Qy 179 WPPPSGADPAPWLPSPGRRRRRTAFASRHGRKHGKSRKLRCSKKPLHVNFKELGWDWI 238
Db 363 -----VVEYLFQ-SRRKRAPLNRQGRKPRSKNLKARCSRKALHVNFKDMGWDWI 412

Qy 239 IAPLEYAYHCEGVCDFPLRSHLEPTNHAIOTLNSMDPGSTPPSCVPKLTPTISILY 298
Db 413 IAPLEYAFHCEGLCEFFPLRSHLEPTNHAVIOTLNSMDPESTPTCCVPTPLRSLISILF 472

Qy 299 IDAGNNVYKQYEDMVVESCGR 321
Db 473 IDSANNVYKQYEDMVVESCGR 495

RESULT 4
GDF6_MOUSE
ID GDF6_MOUSE STANDARD; PRT; 125 AA.
AC P43026;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Growth/differentiation factor 6 precursor (GDF-6) (Fragment).
GN GDF6 or GDF-6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C; TISSUE=Liver;
RX MEDLINE=94195427; PubMed=8145850;
RA Storm E.E., Huynh T.V., Copeland N.G., Jenkins N.A., Kingsley D.M.,
RA Lee S.-J.;
RT "Limb alterations in brachypodism mice due to mutations in a new
RL Nature 368:639-643(1994).
CC -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation

```

CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U08338; AAA18779.1; -
DR HSSP; P12643; 3BMP.
DR MGI; 95689; Gdf6.
DR InterPro; IPR001839; TGF-beta.
DR Pfam; PF00019; TGF-beta; 1.
DR ProDom; PD000357; TGF-beta; 1.
DR SMART; SM00204; TGF-beta; 1.
DR PROSITE; PS00250; TGF-BETA_1; 1.
KW Growth factor; Cytokine; Glycoprotein.
FT NON_TER 1
FT PROPEP <1 5
FT CHAIN 6 125
FT DISULFID 24 90
FT DISULFID 53 122
FT DISULFID 57 124
FT DISULFID 89 89
FT INTERCHAIN (BY SIMILARITY).
FT SEQUENCE 125 AA; 14373 MW; 10FA2A5B7748DA32 CRC64;

Query Match 39.38; Score 691; DB 1; Length 125;
Best Local Similarity 99.28; Pred. No. 4.9e-44;
Matches 124; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 197 RRRRTAFASRGRKRGKSRKPLHVNFKELGWDWIIAPLEYAYHCEGVCDFF 256
DB 1 RRRRTAFASRGRKRGKSRKPLHVNFKELGWDWIIAPLEYAYHCEGVCDFF 60
QY 257 LRSHLEPTNHAIQTLMNSMDPGSTPPSCCVPTKLTPTISILYIDAGNNVYKQYEDMVVE 316
DB 61 LRSHLEPTNHAIQTLMNSMDPGSTPPSCCVPTKLTPTISILYIDAGNNVYKQYEDMVVE 120
QY 317 SCGR 321
DB 121 SCGR 125

RESULT 5
ID GDF7_MOUSE STANDARD; PRT; 151 AA.
AC P43029;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Growth/differentiation factor 7 precursor (GDF-7) (Fragment).
OS GDF7 OR GDF-7.
OC Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BAUB/C; TISSUE=Liver;
RA MEDLINE=94195427; PubMed=8145850;
RA Storm E.E., Huynh T.V., Copeland N.G., Jenkins N.A., Kingsley D.M.,
RA Lee S.-J.;
RT "Limb alterations in brachypodism mice due to mutations in a new
RT member of the TGF-beta-superfamily";
RL Nature 368:639-643(1994).
CC -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC

Query Match 31.2%; Score 549; DB 1; Length 151;
Best Local Similarity 59.5%; Pred. No. 1.3e-33;
Matches 103; Conservative 13; Mismatches 35; Indels 22; Gaps 1;
QY 149 RSQRKNLFAMREQLGSAEAGPCAGAGSWPPSPGADPARDPWLSPGRRRRRTAFASRH 208
DB 1 RRRRTALACTGAQSGGGGGGGGGGGGGGGA----- 38
QY 209 GKRHGKSRKLRCKKPLHVNFKELGWDWIIAPLEYAYHCEGVCDFFPLRSHLEPTNHAI 268
DB 39 GRGRRGRGRCSRKSLHVDVKELGWDWIIAPLEYAYHCEGVCDFFPLRSHLEPTNHAI 98
QY 269 IQTLMSMDPGSTPPSCCVPTKLTPTISILYIDAGNNVYKQYEDMVVEGCGCR 321
DB 99 IQTLMSMDPGSTPPSCCVPTKLTPTISILYIDAGNNVYKQYEDMVVEGCGCR 151

RESULT 6
ID BMPA_XENLA STANDARD; PRT; 398 AA.
AC P25703;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Bone morphogenetic protein 2-1 precursor (BMP-2-1).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=91274367; PubMed=2054389;
RA Plessow S., Koester M., Knoechel W.;
RT "cDNA sequence of Xenopus laevis bone morphogenetic protein 2
RT (BMP-2).";
RL Biochim. Biophys. Acta 1089:280-282(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC MEDLINE=92378616; PubMed=1510675;
RA Nishimatsu S., Suzuki A., Shoda A., Murakami K., Ueno N.;
RT "Genes for bone morphogenetic proteins are differentially transcribed
RT in early amphibian embryos";
RL Biochem. Biophys. Res. Commun. 186:1487-1495(1992).
CC -!- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION.
CC -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC

the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

EMBL: X55031; CAA38850.1; -
 EMBL: X63424; CAA45018.1; -
 PIR: S16244; S16244.
 PIR: JH0687; JH0687.
 HSSP: P12643; 3BMP.
 InterPro: IPR001839; TGF-beta.
 InterPro: IPR001111; TGF-beta.
 Pfam: PF00688; TGF-beta; 1.
 Pfam: PF00688; TGF-beta; 1.
 SMART: SM00204; TGF-beta; 1.
 SMART: SM00250; TGF-beta; 1.
 Signal: Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
 SIGNAL: 1 23 POTENTIAL.
 CHAIN 24 284 BONE MORPHOGENETIC PROTEIN 2-I.
 FT DISULFID 298 363 BY SIMILARITY.
 FT DISULFID 327 395 BY SIMILARITY.
 FT DISULFID 331 397 BY SIMILARITY.
 FT DISULFID 362 362 INTERCHAIN (BY SIMILARITY).
 FT CARBOHYD 137 137 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 202 202 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 340 340 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CONFLICT 7 7 S -> P (IN REF. 2).
 FT CONFLICT 16 16 V -> L (IN REF. 2).
 FT CONFLICT 233 233 N -> T (IN REF. 2).
 SQ SEQUENCE 398 AA; 45575 MW; 150AC64A47D2E15F CRC64;

Query Match 24.3%; Score 426.5; DB 1; Length 398;
 Best Local Similarity 31.5%; Pred. No. 2.8e-24;
 Matches 105; Conservative 51; Mismatches 88; Indels 89; Gaps 13;

QY 12 OKYLFVDSMLSDKEELVGAELRFRQAPSWPGPPAGPLH-VOLFCLSP-----61

Db 132 QREFFNLSSIPNEELVTSALRIFRQVQEPFSDSKLHRINIVDIVKPAASRGV 191

QY 62 -LLDARTLDPOGAPGAGVEFVWQGL-----RHQPKQLCLLEAANGELDAGEA 115

Db 192 ELDTLRIHNN-----ESKWSFDTVPATRIAHKQPNHGFVEV-----NHL 236

QY 116 EGPQPPPPDLRLSLGFGRRV-----PQRALLVFTSRQKNLFAEMREQLGSA 170

237 -NDKNVKKHVR-----ISRLTPDKDNWQIRPLLVTFSD-----G 273

QY 171 PGAGSGSNPPSPGAPDARPLSPGRRRRRTAFASRHGRHKKSLR--CSKKPLH 228

Db 274 EHALH-----KROKQA-----RHQKRLKSSCRHPLYVD 306

QY 229 FRLGWDWIIAPLEYAYHCEGVDPLRLSHLEPTNHAIIOTLMSMDPGSTPPSC 288

Db 307 FSDVGNDWIVAPPGYHAFYCHGECPPPLADHLNSTNHAIVQTLVNSVNT-NIPK 365

QY 289 YLTPISILYIDAGNNVYKQYEDMVVESCGR 321

Db 366 YLSAISMLYLDENEKVLKNYQDMVVEGCGCR 398

RESULT 7

ID BMPB XENLA STANDARD; PRT; 398 AA.

AC P30884;

DT 01-JUL-1993 (Rel. 26, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DE Bone morphogenetic protein 2-II precursor (BMP-2-II).

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Piploidea; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;

RN SEQUENCE FROM N.A.

RX MEDLINE-92378616; PubMed-1510675;

RT Nishimatsu S., Suzuki A., Shoda A., Murakami K., Ueno N.;

RA "Genes for bone morphogenetic proteins are differentially transcribed

in early amphibian embryos.";

RL Biochem. Biophys. Res. Commun. 186:1487-1495(1992).

CC -!- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION.

CC -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.

CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

between the Swiss Institute of Bioinformatics and the EMBL outstation -

the European Bioinformatics Institute. There are no restrictions on its

use by non-profit institutions as long as its content is in no way

modified and this statement is not removed. Usage by and for commercial

entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

or send an email to license@isb-sib.ch).

EMBL: X63425; CAA45019.1; -

PIR: JH0688; JH0688.

HSSP: P12643; 3BMP.

InterPro: IPR001839; TGF-beta.

InterPro: IPR001111; TGF-beta.

Pfam: PF00019; TGF-beta; 1.

Pfam: PF00688; TGF-beta; 1.

ProDom: PD000357; TGF-beta; 1.

SMART: SM00204; TGF-beta; 1.

PROSITE: PS00250; TGF-beta; 1.

Signal: Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.

SIGNAL: 1 23 POTENTIAL.

FT CHAIN 24 284 POTENTIAL.

FT DISULFID 298 363 BONE MORPHOGENETIC PROTEIN 2-II.

FT DISULFID 327 395 BY SIMILARITY.

FT DISULFID 331 397 BY SIMILARITY.

FT DISULFID 362 362 INTERCHAIN (BY SIMILARITY).

FT CARBOHYD 137 137 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 202 202 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 237 237 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 340 340 N-LINKED (GLCNAC. .) (POTENTIAL).

SQ SEQUENCE 398 AA; 45616 MW; 60B41FA2C8E603DC CRC64;

Query Match 24.3%; Score 426.5; DB 1; Length 398;
 Best Local Similarity 31.3%; Pred. No. 2.8e-24;
 Matches 104; Conservative 51; Mismatches 90; Indels 87; Gaps 12;

QY 12 OKYLFVDSMLSDKEELVGAELRFRQAPSWPGPPAGPLH-VOLFCLSP-----61

Db 132 QREFFNLSSIPNEELVTSALRIFRQVQEPFSDSKLHRINIVDIVKPAASRGV 191

QY 62 -LLDARTLDPOGAPGAGVEFVWQGL-----RHQPKQLCLLEAANGELDAGEA 115

Db 192 ELDTLRIHNN-----ESKWSFDTVPATRIAHKQPNHGFVEV-----NHL 248

QY 116 RGPQPPPPDLRLSL-----GFRGRVPPQERALLVFTSRQKNLFAEMREQLGSA 171

Db 249 S-----RSLTLDKGHWPRIP-----LLVTFSD-----GK 274

QY 172 GAGAGSNPPSPGAPDARPLSPGRRRRRTAFASRHGRHKKSLR--CSKKPLH 229

Db 275 EHALH-----KROKQA-----RHQKRLKSSCRHPLYVD 307

QY 230 KELGWDWIIAPLEYAYHCEGVDPLRLSHLEPTNHAIIOTLMSMDPGSTPPSC 289

Db 308 FSDVGNDWIVAPPGYHAFYCHGECPPPLADHLNSTNHAIVQTLVNSVNT-NIPK 366

QY 290 YLTPISILYIDAGNNVYKQYEDMVVESCGR 321

DB 367 ELASLSMLYLDENKVKLVKNYQDMVVEGCGCR 398

RESULT 8

BMP4_CHICK

ID BMP4_CHICK STANDARD; PRT: 405 AA.

AC O90752;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Bone morphogenetic protein 4 precursor (BMP-4).

GN BMP4 OR BMP-4.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

NCBI_TaxID=9031;

RN [1]

RN SEQUENCE FROM N.A.

RP STRAIN-WHITE LECHORN;

RC MEDLINE=94163974; PubMed=8119128;

.X Francis P.H., Richardson M.K., Brickell P.M., Tickle C.;

.AT "Bone morphogenetic proteins and a signalling pathway that controls

.RT patterning in the developing chick limb.";

.RL Development 120:209-218(1994).

RN [2]

RP FUNCTION.

RP MEDLINE=99128179; PubMed=927590;

RX Pizette S., Niswander L.;

RA "BMPs negatively regulate structure and function of the limb apical

RT ectodermal ridge.";

RL Development 126:883-894(1999).

CC CC

CC -!- FUNCTION: NEGATIVELY REGULATES THE STRUCTURE AND FUNCTION OF THE

CC LIMB APICAL ECTODERMAL RIDGE.

CC -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).

CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

CC

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announcement/>

CC or send an email to license@isb-sib.ch).

CC

EMBL; X75915; CAA53514.1; -.

DR HSPSP; P12643; 3BMP.

DR InterPro; IPR001839; TGF-beta.

DR InterPro; IPR001111; TGFb_N.

.R Pfam; PF000019; TGF-beta; 1.

.R Pfam; PF00688; TGFb_propeptide; 1.

DR ProDom; PD000357; TGF-beta; 1.

DR SMART; SM00204; TGFb; 1.

DR PROSITE; PS00250; TGF_BETA_1; 1.

KW Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.

FT SIGNAL 1 19 POTENTIAL.

FT PROPEP 20 291 BY SIMILARITY.

FT CHAIN 292 405 BONE MORPHOGENETIC PROTEIN 4.

FT FT DISULFID 305 370 BY SIMILARITY.

FT FT DISULFID 334 402 BY SIMILARITY.

FT FT DISULFID 338 404 BY SIMILARITY.

FT FT DISULFID 369 369 INTERCHAIN (BY SIMILARITY).

FT FT CARBOHYD 144 144 N-LINKED (GLCNAC. .) (POTENTIAL).

FT FT CARBOHYD 208 208 N-LINKED (GLCNAC. .) (POTENTIAL).

FT FT CARBOHYD 347 347 N-LINKED (GLCNAC. .) (POTENTIAL).

FT FT CARBOHYD 362 362 N-LINKED (GLCNAC. .) (POTENTIAL).

SEQ SEQUENCE 405 AA; 46057 MW; 544302DBA0A40F81 CRC64;

Query Match 23.8%; Score 418.5; DB 1; Length 405;

Best Local Similarity 31.8%; Pred. No. 1.1e-23;

Matches 104; Conservative 47; Mismatches 101; Indels 75; Gaps 11;


```
QY 230 KELGWDWIIAPLEYEAYHCEGVCDFPLRSHLEPTNHAIQITLMSMDPGSTPPSCCVPT 289
Db 361 RDLGQMDWIIAPLEYEAYHCEGVCDFPLRSHLEPTNHAIQITLMSMDPGSTPPSCCVPT 420
QY 290 KLTPTISILYIDAGNNVYKQYEDMVVSCGC 320
Db 421 KLNATSVLYFDSSNVILKRYNMVVRSCGC 451

RESULT 11
DVR1_STRPU STANDARD; PRT; 461 AA.
AC P48969;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE DVR-1 protein homolog precursor.
GN DVR1.
OS Strongylocentrotus purpuratus (Purple sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
NC Echinoidea; Euechinoidea; Echinacea; Echinoidea; Strongylocentrotidae;
C Strongylocentrotus.
JX NCBI_TaxID=7668;
RN [1]
SEQUENCE FROM N.A.
RA Ponce M.R., Nicol J.L., Davidson E.H.;
RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
CC -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (PROBABLE).
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; Z48313; CAA88306.1; -.
CC HSSP; P18075; 1BMP.
CC InterPro; IPR002400; GF_cysknot.
CC InterPro; IPR001839; TGF-beta.
CC InterPro; IPR001111; TGFb_N.
CC Pfam; PF00019; TGF-beta; 1.
CC Pfam; PF00688; TGFb_propeptide; 1.
CC PRINTS; PR00438; GFCYSKNOT.
CC PRODOM; PD000357; TGF-beta; 1.
CC SMART; SM00204; TGFb; 1.
CC PROSITE; PS00250; TGF_BETA_1; 1.
CC Growth factor; Cytokine; Glycoprotein; Signal.
CC SIGNAL 1 30 POTENTIAL.
CC PROPEP 31 338 POTENTIAL.
CC CHAIN 339 461 DVR-1 PROTEIN HOMOLOG.
CC DISULFID 360 426 BY SIMILARITY.
CC DISULFID 389 458 BY SIMILARITY.
CC DISULFID 393 460 BY SIMILARITY.
CC DISULFID 425 425 INTERCHAIN (BY SIMILARITY).
CC CARBOHYD 149 149 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 402 402 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SEQUENCE 461 AA; 51881 MW; 2573D54B6625F7EF CRC64;

Query Match 23.1%; Score 405.5; DB 1; Length 461;
Best Local Similarity 32.4%; Pred. No. 1.1e-22;
Matches 108; Conservative 42; Mismatches 104; Indels 79; Gaps 12;

QY 13 KYLFVSMLSKEELVGAELRFRQAPSAPWGPAGPLHVQLF-----PCLSPILLDAR 66
Db 182 RYREDIGRIPOGETVTSALRVRFDRA--GQGRSLYRIDVLLRERGSDGRSPVYLDST 239
QY 67 TLDPOGAPPAGWEVDFV-----WQGLRHOPWQKLCLELRANGELDAGEAEARGPQQ 120
Db 240 IV---GAGDGHGWLVFDMTSATSTW---RSYPGANVGLQLRVE---SLQGLNID----- 283
```

```
QY 121 PPPDLRLSGFGRVRPPQBRALLVYVTRSQ-----RKNLFAEMRQLGSABAACP 171
Db 284 --PTDAGVGVGN--NEGREFPMVVFQRRNEEVATNHLRRNRRAATROKKG----- 332
QY 172 GAGAEWSGPPPGAPDARPLSPGRRRRR---TAFASRHGRKRGKSLRCSKKPLHW 227
Db 333 -----GKRPRKPTDNDIASR-DSASLSNDSMDQCKRKNLFV 367
QY 228 NFRELGWDDWIIAPLEYEAYHCEGVCDFPLRSHLEPTNHAIQITLMSMDPGSTPPSCCV 287
Db 368 NFEDLDWQWIIAPLEYEAYHCEGVCDFPLRSHLEPTNHAIQITLMSMDPGSTPPSCCV 427
QY 288 PTKLTPTISILYIDAGNNVYKQYEDMVVSCGC 320
Db 428 PTKLSPTVLYDDSRNVVLKRYNMVVRACGC 460

RESULT 12
BMP2_RABIT STANDARD; PRT; 395 AA.
AC O46584;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Bone morphogenetic protein 2 precursor (BMP-2).
GN BMP2 OR BMP-2.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
NC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
JX NCBI_TaxID=9986;
RN [1]
SEQUENCE FROM N.A.
RA STRAIN-NEW ZEALAND WHITE; TISSUE=Ocular ciliary epithelium;
RA Wan X.L., Sears J., Chen S.;
RT "Cloning and expression of BMP-2/-4 from rabbit ocular ciliary
RT epithelium."
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION (BY SIMILARITY).
CC -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF041421; AAB96785.1; -.
CC HSSP; P12643; 3BMP.
CC InterPro; IPR002405; Inhibin_alpha.
CC InterPro; IPR001839; TGF-beta.
CC InterPro; IPR001111; TGFb_N.
CC Pfam; PF00019; TGF-beta; 1.
CC Pfam; PF00688; TGFb_propeptide; 1.
CC PRINTS; PR00669; INHIBINA.
CC PRODOM; PD000357; TGF-beta; 1.
CC SMART; SM00204; TGFb; 1.
CC PROSITE; PS00250; TGF_BETA_1; 1.
CC Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
CC SIGNAL 1 23 POTENTIAL.
CC PROPEP 24 281 BY SIMILARITY.
CC CHAIN 282 395 BONE MORPHOGENETIC PROTEIN 2.
CC DISULFID 295 360 BY SIMILARITY.
CC DISULFID 324 392 BY SIMILARITY.
CC DISULFID 328 394 BY SIMILARITY.
CC DISULFID 359 359 INTERCHAIN (BY SIMILARITY).
CC CARBOHYD 134 134 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 199 199 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 337 337 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SEQUENCE 395 AA; 44664 MW; 8D1DDCFBAC582496 CRC64;
```

```
Query Match      23.0%; Score 403.5; DB 1; Length 395;
Best Local Similarity 30.5%; Pred. No. 1.3e-22;
Matches 100; Conservative 51; Mismatches 98; Indels 79; Gaps 12;

QY 12 QKYLFDVSMLSKDELVAELRQAPSPAGPLH-VQLPCLSP----- 61
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 129 RRFNLTISIPPEFTISAELOVFREQOEALGDDSGFHRINIYEIKPATANSKFPAT 188
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 62 -LLDARTLDPOGAPAGVDFVWGLRHQPWKQLCLLELRANGELDAEARGPQQ 120
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 189 RLUDRLVQN---TSRWESFDVTPAVMR--W-----TAQGHANHFV-VEVTHLEE 234
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 121 PPPDLRLSLGFGRRVP-----PQERALLVYFTRSQKRLFAEMREQLGSAEAGPGAGA 175
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 235 KQGVSKRHVRISLHSDHESQIRPLLVTF-----G-----GH 268
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 176 EGSNPPSGAPARWLPSPGRRRTAFASRHGRHKKSLR--CSKKPLHVNFKELG 233
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
269 DKGKPLH-----RREKRA-----KHKRKLKSKCRHPLVDFSDVG 308
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 234 WDDTIIAPLEYEAYHCEGVCDPLSLHLEPTNHAIQTLNMSMDPGSPCCVPTKLT 293
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 309 WNDMIVAPCYHAFYCHGCEPPLADHLNSTNHAIVQTLVNSV-SKIPKACCVPTLSA 367
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 294 ISLIIIDAGNNVYKQYEDMVVSGCR 321
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 368 ISMLIDMEKVKLVKNYODMVVSGCR 395
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 13
BMP2_RAT      STANDARD;      PRT;      393 AA.
ID BMP2_RAT
AC P49001;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Bone morphogenetic protein 2 precursor (BMP-2) (BMP-2A).
GN BMP2 OR BMP-2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone;
Feng J.O., Chen D., Feng M., Harris M.A., Mundy G.R., Harris S.E.;
Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.
-!- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION.
-!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.
-!- TISSUE SPECIFICITY: FEMUR, CALVARIA, TRACHEA, LUNG AND OVARY.
-!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Z25868; CAA81088.1;
DR HSSP; P12643; 3BMP.
DR InterPro; IPR001839; TGF-beta.
DR InterPro; IPR001111; TGFb.N.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb.propeptide; 1.
DR ProDom; PD000357; TGF-beta; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF-BETA_1; 1.
DR Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
FT SIGNAL 1 19 POTENTIAL.
```

```
FT PROPEP      20 279
FT CHAIN       280 393
FT DISULFID    293 358
FT DISULFID    322 390
FT DISULFID    326 390
FT DISULFID    337 357
FT CARBOHYD    133 133
FT CARBOHYD    161 161
FT CARBOHYD    197 197
FT CARBOHYD    335 335
SO SEQUENCE    393 AA; 44383 MW; 7D20865852E0F213 CRC64;

Query Match      22.8%; Score 401; DB 1; Length 393;
Best Local Similarity 30.8%; Pred. No. 2e-22;
Matches 105; Conservative 50; Mismatches 98; Indels 88; Gaps 13;

QY 2 SLSHTPLRROKYLFVDSMLSDKEELVGAELRQAPSPAGPLHVLVOLPCLSP 61
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 120 SEMSGKTSRR--FFFNLSVPTDFLTSAELQIFREQMQLGNSFQHRINIYEIKPA 177
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 62 -----LLDARTLDPOGAPAGVDFVWGLRHQPWKQLCLLELRANGELDAE 111
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 178 TASSKFPVTRLLDRLVTQN---TSQWESFDVTPAVMR--W-----TAQGHANHFV 224
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 112 EARARGPOPPPPDLRLSLGFGRRVRPQERALLVYFTRSQKRLFAEMREQLGSAEAGP 171
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 225 VEVAHLEKP-----GVSKR-----HVRISRLHQD----- 250
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 172 GAGAECSWPPSPGADARPMLPSG-----RRRRRTAFASRHGRHKKSLR--C 220
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 251 ----EHSW-----SQVRPLLVTFCHDGKGPLHKKRQA-----KHKRKLKSSC 293
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 221 SKKPLHVNFKELGDDWIIAPLEYEAYHCEGVCDPLSLHLEPTNHAIQTLNMSMDPGS 280
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 294 KRHLIYDFSDVGNWDIIVAPPGYHAFYCHGCEPPLADHLNSTNHAIVQTLVNSV-SK 352
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 281 TPPSCCVPTKLTPTISILYIDAGNNVYKQYEDMVVSGCR 321
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 353 IPKACCVPTLSAISMLYLDENEKVKLVKNYODMVVSGCR 393
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 14
BMP4_MOUSE     STANDARD;      PRT;      408 AA.
ID BMP4_MOUSE
AC P21275;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Bone morphogenetic protein 4 precursor (BMP-4) (BMP-2B).
GN BMP4 OR BMP-4 OR DVR-4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Dickinson M.E., van der Meer-De Jong R., Hogan B.L.M.;
RL Submitted (XXX-1992) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=9328203; PubMed=8507180;
RA Kurihara T., Kitamura K., Takaoka K., Nakazato H.;
RT "Murine bone morphogenetic protein-4 gene: existence of multiple
RL Biochem. Biophys. Res. Commun. 192:1049-1056(1993).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=93365172; PubMed=8358941;
RA Takaoka K., Yoshikawa H., Hasimoto J., Masuhara K., Miyamoto S.,
RA Suzuki S., Ono K., Matsui M., Oikawa S., Tsuruoka N.;
RT "Gene cloning and expression of a bone morphogenetic protein derived
RT from a murine osteosarcoma.";
RN [4]
```

RL RN SEQUENCE FROM N.A.
 RC STRAIN=129/SV; TISSUE=Liver;
 RX MEDLINE=96081880; PubMed=7499338;
 RA Feng J.Q., Chen D., Cooney A.J., Tsai M., Harris M.A., Tsai S.Y.,
 RA Mundy G.R., Harris S.E.;
 RT "The mouse bone morphogenetic protein-4 gene. Analysis of promoter
 RT utilization in fetal rat calvarial osteoblasts and regulation by
 RT COUP-TFI orphan receptor.";
 RL J. Biol. Chem. 270:28364-28373(1995).
 [5]
 RN SEQUENCE OF 241-408 FROM N.A.
 RP MEDLINE=90228966; PubMed=1970330;
 RA Dickinson M.E., Robrin M.S., Silan C.M., Kingsley D.M., Justice M.J.,
 RA Miller D.A., Ceci J.D., Lock L.F., Lee A., Buchberg A.M.,
 RA Siracusa L.D., Lyons K.M., Derynck R., Hogan B.L.M., Copeland N.G.,
 RA Jenkins N.A.;
 RT "Chromosomal localization of seven members of the murine TGF-beta
 RT superfamily suggests close linkage to several morphogenetic mutant
 RT loci.";
 Genomics 6:505-520(1990).
 CC -!- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION.
 CC -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: SECRETED INTO THE EXTRACELLULAR MATRIX.
 CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: X56848; CAA40179.1; -
 CC EMBL: S65032; AAB28021.1; -
 CC EMBL: I47480; AAC37698.1; ALT_INIT.
 CC EMBL: D14814; BAA03555.1; -
 CC PIR: B34201; B34201.
 CC PIR: S29523; S29523.
 CC HSP: P12643; 3BMP.
 CC MGD: MGI:88180; Bmp4.
 CC InterPro: IPR001839; TGF-beta.
 CC InterPro: IPR001111; TGFb_N.
 CC Pfam: PF00019; TGF-beta; 1.
 CC Pfam: PF00688; TGFb_propeptide; 1.
 CC ProDom: PD000357; TGF-beta; 1.
 CC SMART: SM00204; TGFb; 1.
 CC PROSITE: PS00250; TGF_BETA_1; 1.
 CC Signal: Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
 CC SIGNAL: 1 19 POTENTIAL.
 CC PROPEP 20 292
 CC CHAIN 293 408 BONE MORPHOGENETIC PROTEIN 4.
 CC FT CHAIN 293 408 BY SIMILARITY.
 CC FT DISULFID 308 373 BY SIMILARITY.
 CC FT DISULFID 337 405 BY SIMILARITY.
 CC FT DISULFID 341 407 BY SIMILARITY.
 CC FT DISULFID 372 372 INTERCHAIN (BY SIMILARITY).
 CC FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 209 209 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 350 350 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 365 365 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CONFLICT 407 407 C -> S (IN REF. 2).
 CC SEQUENCE 408 AA: 46496 MW: 350530844624EF9D CRC64;
 Query Match 22.8%; Score 401; DB 1; Length 408;
 Best Local Similarity 31.5%; Pred. No. 2.1e-22;
 Matches 105; Conservative 42; Mismatches 98; Indels 88; Gaps 10;
 QY 13 KYFDVSMLSKDEELVGAELRFR-----QAPSAPWG-----PPAG--PLHVQLF 55
 Db 140 RFLFNLSIPENEIVSSALRLRFRQVDGPDWEGFHRINIEYVWKPPAENVPGH---- 195

QY 56 PCLSPLLILDARTLDPOGAPPAGWVFVWQGLRHQPWKQLCLELRAANGELDAGAEARA 115
 Db 196 --LITRLDTRLVHHN---VTRWETFV----- 218
 QY 116 RGPOQPPPPDLSGLGFRGRRVRPPQERALLVVVTRSORKNLFAEMREQLGSAEAAAGGAGA 175
 Db 219 -----SPAVLR---WTRKQPNVGLAIEVTHLQTRTHQGOHVRISSRLPQGSANA-- 267
 QY 176 EGSWPPPPSGADPARPWLPSGCR-----RRRTAFASRHGKRGKSRRLRCSKGLHVN 228
 Db 268 -----QLRPLLVTFCHDGRGHTLRRRAKRSKPKHHQPORSKKNKNCRRSLYVD 316
 QY 229 PKELCWDDWIIAPLEYEAYHCEGVCDFPLRSHLEPTNHAIIQIOLMNSMDPGSPFSCVCP 288
 Db 317 FSDVGWDMVIAPPGYQAFYCHGCPPLADHLNSTNHAIVQTLVNSVN-SSIRSCCVCP 375
 QY 289 TKLPISILYIDAGNNVYKQYEDMWVSCGR 321
 Db 376 TELSALMILYDEYDKVVKYQEMVVEGCGCR 408
 RESULT 15
 BMP4_RABIT
 ID BMP4_RABIT STANDARD; PRT; 409 AA.
 AC O46576;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Bone morphogenetic protein 4 precursor (BMP-4).
 GN BMP4 OR BMP-4.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RC SEQUENCE FROM N.A.
 RC STRAIN=NEW ZEALAND WHITE; TISSUE=Ocular ciliary epithelium;
 RA Wan X.L., Sears J., Chen S., Sears M.;
 RT "Cloning and expression of BMP-2/-4 from rabbit ocular ciliary
 RT epithelium.";
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION (BY SIMILARITY).
 CC -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: SECRETED INTO THE EXTRACELLULAR MATRIX.
 CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: AF042497; AAB97467.1; -
 CC HSP: P12643; 3BMP.
 CC InterPro: IPR001839; TGF-beta.
 CC InterPro: IPR001111; TGFb_N.
 CC Pfam: PF00019; TGF-beta; 1.
 CC Pfam: PF00688; TGFb_propeptide; 1.
 CC ProDom: PD000357; TGF-beta; 1.
 CC SMART: SM00204; TGFb; 1.
 CC PROSITE: PS00250; TGF_BETA_1; 1.
 CC Signal: Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
 CC SIGNAL: 1 19 POTENTIAL.
 CC PROPEP 20 293 BY SIMILARITY.
 CC CHAIN 294 409 BONE MORPHOGENETIC PROTEIN 4.
 CC FT DISULFID 309 374 BY SIMILARITY.
 CC FT DISULFID 338 406 BY SIMILARITY.
 CC FT DISULFID 342 408 BY SIMILARITY.
 CC FT DISULFID 373 373 INTERCHAIN (BY SIMILARITY).
 CC FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).

```

FT CARBOHYD 209      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 351      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 366      N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 409 AA; 46641 MW; 35557561447AD625 CRC64;

Query Match      22.7%; Score 398.5; DB 1; Length 409;
Best Local Similarity 31.4%; Pred. No. 3.2e-22;
Matches 105; Conservative 42; Mismatches 98; Indels 89; Gaps 10;

QY 13 KYLFVMSLSDEELVGAEELRFR-----QAPSAPWG-----PPAG--PLHVOLF 55
Db 140 RFLFNLSIPENEAISAEELRFRQVQDQDWERGFHRINIYEVMPKPPAEAVPGH---- 195
QY 56 PCLSPILLIDARTLDPOGAPPAGWEVFDVWQGLRHPQWQLCLELRAANGELDAGEAEARA 115
Db 196 --LITRLDTRLVHN---VTRWETFDV----- 218
QY 116 RGPQQPPPPDLRLSLGFRVRPPQERALLVVFTRSORKNLFAEMREQLGSAEAGPGAGA 175
Db 219 -----SPAVLR---WTRKQPNHGLAVEVTHFHTTRTHQGHVRLSRSLQGGSDWA-- 267
QY 176 EGSWPPPGADARPWLPSGR-----RRRTAFASRHGKHKSRLCRCKKPLHV 227
Db 268 -----QFRPLLVTFGHDGRGHALTERRRAKRSKHHHPQARAKKNCRRHALYV 316
QY 228 NFKELGNDWIIITAPLEYAHCEGVCDPPLRSHLEPTNHAIIQTLNMSMDPGSTPPSCCV 287
Db 317 DFDVGNDWIVAPFGYQAFYCHGDCPPFLADHFNSTNHAIVQTLVNSVN-SSIPKACCV 375
QY 288 PTKLTPISILYIDAGNNVYKQYEDMVYESGCCR 321
Db 376 PTELSAISMLYLDYDKVKVKNYQEMVEGCGCR 409

```

Search completed: October 3, 2002, 15:46:00
Job time: 406 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 3, 2002, 15:45:36 ; Search time 48.58 Seconds
(without alignments)
1143.091 Million cell updates/sec

Title: US-09-945-182-26

Perfect score: 1757

Sequence: 1 NSDLSHPTLRQKYLFDVSM.....GNVVYKQYEDMVVSCGCR 321

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

al number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_19:*
1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteria:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1000.5	56.9	399	13 Q9W753	Q9W753 xenopus lae
2	907	51.6	412	13 O12938	O12938 brachydanio
3	796	45.3	447	6 Q9BDW8	Q9BDW8 cercopithec
4	782	44.5	413	13 Q9DGN4	Q9DGN4 xenopus lae
5	771	43.9	501	4 Q96SBL	Q96SBL homo sapien
6	756	43.0	500	13 Q9W6G0	Q9W6G0 gallus gall
7	737	41.9	294	6 Q9BDW9	Q9BDW9 macaca fasc
8	712	40.5	324	13 Q9YHW9	Q9YHW9 gallus gall
9	698.5	39.8	261	13 Q9W6C0	Q9W6C0 brachydanio
10	664.5	37.8	257	13 O42303	O42303 brachydanio
11	634	36.1	441	11 Q99MV1	Q99MV1 mus musculu
12	612.5	34.9	126	13 Q93573	Q93573 gallus gall
13	451	25.7	277	13 Q90Y82	Q90Y82 lampetra ja
14	427.5	24.3	417	5 Q9XYQ7	Q9XYQ7 lytechinus
15	426	24.2	289	5 Q9XYQ8	Q9XYQ8 strongyloce
16	423.5	24.1	398	13 Q90YD7	Q90YD7 xenopus tro

17	408	23.2	400	13	O57574	O57574 brachydanio
18	406	23.1	400	13	O13107	O13107 brachydanio
19	405	23.1	364	13	Q9PWK1	Q9PWK1 gallus gall
20	405	23.1	391	13	O90YJ3	O90YJ3 brachydanio
21	402	22.9	301	5	O97390	O97390 crassostrea
22	401.5	22.9	204	5	Q9XZ69	Q9XZ69 tripneustes
23	400.5	22.8	337	6	Q9M2V5	Q9M2V5 canis famil
24	400	22.8	405	5	Q9U588	Q9U588 psychodera
25	399	22.7	361	5	O96504	O96504 brachydanio
26	399	22.7	453	13	P87373	P87373 gallus gall
27	395.5	22.6	411	5	O9U418	O9U418 brachydanio
28	390.5	22.6	128	5	O95W38	O95W38 schistocerc
29	389	22.1	432	13	Q9PTF9	Q9PTF9 brachydanio
30	387	22.0	390	13	Q91597	Q91597 xenopus lae
31	386.5	22.0	411	13	O93369	O93369 brachydanio
32	386	22.0	430	11	O91XF7	O91XF7 mus musculu
33	385.5	21.9	182	13	O90Y81	O90Y81 lampetra ja
34	385.5	21.9	191	5	O26468	O26468 schistocerc
35	384	21.9	313	13	O91403	O91403 gallus gall
36	384	21.9	398	13	O918T6	O918T6 gallus gall
37	381	21.7	614	5	P91720	P91720 drosophila
38	380.5	21.7	178	5	Q25211	Q25211 junonia coe
39	380.5	21.7	411	13	O57573	O57573 brachydanio
40	380	21.6	400	13	O73818	O73818 xenopus lae
41	379	21.6	400	13	O91703	O91703 xenopus lae
42	377.5	21.5	443	5	O76851	O76851 halocynthia
43	374.5	21.3	386	13	O13109	O13109 brachydanio
44	374	21.3	400	13	O90YD6	O90YD6 xenopus tro
45	369	21.0	588	5	O9VQC6	O9VQC6 drosophila

ALIGNMENTS

RESULT 1

Q9W753 ID Q9W753 PRELIMINARY; PRT; 399 AA.
AC Q9W753;
DT 01-NOV-1999 (TRENBLrel. 12, Created)
DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE GROWTH AND DIFFERENTIATION FACTOR 6.
GN GDF6.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoldea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99396700; PubMed=10393114;
RA Chang C., Hemmati-Brivanlou A.;
RT "Xenopus GDF6, a new antagonist of noggin and a partner of BMPs.";
RL Development 126:3347-3357(1999).
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL; AF155125; AAD38402.1; .
DR HSSP; P12643; 3BMP.
DR InterPro; IPR002405; Inhibin_alpha.
DR InterPro; IPR001839; TGF-beta.
DR InterPro; IPR001111; TGFb_N.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR PRINTS; PR00669; INHIBIN.
DR PRODOM; PR000357; TGF-beta; 1.
DR SMART; SM00204; TGFB; 1.
DR PROSITE; PS00250; TGF_BETA; 1.
KW Glycoprotein.
SQ SEQUENCE 399 AA; 45571 MW; C549D973B50B8517 CRC64;

Query Match 56.9%; Score 1000.5; DB 13; Length 399;
Best Local Similarity 63.9%; Pred. No. 2.7e-79;
Matches 205; Conservative 29; Mismatches 54; Indels 33; Gaps 5;


```

Db 241 -PLALRLRGFGWPGGGSAPEERALLVSSRTQRKESLFREMRQAALGAALAAQP--- 296
Qy 175 AEGSWPPSPGAPDARPLWPSGRRRRRTAFASRH-----GKRHGKSRRLRCSKKPL 225
Db 297 -----PPDPGTGTSPRAVTAAGRRRRRTALAGTRTAQSGGGAGRGHGRGRSRSRKPL 351
Qy 226 HVNFKELGWDWIITAPLEYAYHCEGVCDPFLRSHLEPTNHAIQTLMNSMDPGSTPPSC 285
Db 352 HVDFKELGWDWIITAPLDYAYHCEGVCDPFLRSHLEPTNHAIQTLMNSMAPDAAPASC 411
Qy 286 CVPTKLPISILYIDAGNNVYKQYEDMVVESCGR 321
Db 412 CVPARLSPISILYIDAANNVYKQYEDMVVESCGR 447

RESULT 4
Q9DGN4 PRELIMINARY; PRT; 413 AA.
Q9DGN4;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE GROWTH/DIFFERENTIATION FACTOR 16 PRECURSOR PROTEIN.
GN GDF16.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
CC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20368184; PubMed=10906478;
RA Vokes S.A., Krieg P.A.;
RT "Gdf16, a novel member of the growth/differentiation factor subgroup
RT of the TGF-beta superfamily, is expressed in the hindbrain and
RT epibranchial placodes."
RL Mech. Dev. 95:279-282(2000).
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL; AF239676; AAF99597.1;
DR HSP; P12643; 3BP.
DR InterPro; IPR001839; TGF-beta.
DR InterPro; IPR001111; TGFb.N.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGF-beta; 1.
DR ProDom; PD000357; TGF-beta; 1.
DR SMART; SM00204; TGF-beta; 1.
DR PROSITE; PS00250; TGF-BETA; 1.
DR Glycoprotein; Signal.
DR SIGNAL 1 23
SQ SEQUENCE 413 AA; 46510 MW; 5F1B0D7D97E591F6 CRC64;

Query Match 44.5%; Score 782; DB 13; Length 413;
Best Local Similarity 51.2%; Pred. No. 3.2e-60;
Matches 170; Conservative 41; Mismatches 83; Indels 38; Gaps 10;

Qy 1 NSDSLHTPLRQKYLFDVSMISDKELVGAEELRFRQAP--SAPWPPAGPLHVQLFPC- 57
Db 109 HDDLPQK-PEQKFLDTRSPERDEIVGAEELRFRFPEDTSSISGSLVHLNLYTCP 167
Qy 58 ---LSPLLDARTLDPOGAPAGVEFDVQ--GLRHOPWKQLCLELRAANGELDAGEAE 112
Db 168 TGWEQPKLIDSRADLLDTVFESKVEFVNWKAVGNRRLSGETLCLFMKI-----VSDIK 221
Qy 113 ARAGPQQPPPLDLRSLGFRVRPPQERALLVFTSRQK-NLFAEMRQOLGSAEAGP 171
Db 222 ATAFEPVQ-----IGFSREGOLPHEKALLVSSHSKRENLFKEIROKIKSI----- 268
Qy 172 GAGAGSWPPSPGAPDARPLWPSGRRRRRTAFASR--HGRHKGKSRRLRCSKKPLHVNF 229
Db 269 -GNPKFLEPPSPGQGSQSTAK-----RRWKRTTLPTRTNNGKGHAKSKTRCSKKPLLVNF 321
```

```

Qy 230 KELGWDWIITAPLEYAYHCEGVCDPFLRSHLEPTNHAIQTLMNSMDPGSTPPSCCVPT 289
Db 322 KELGWDWIITAPLDYAYHCEGVCDPFLRSHLEPTNHAIQTLMNSMDPESTPPSCCVPS 381
Qy 290 KLPISILYIDAGNNVYKQYEDMVVESCGR 321
Db 382 KLSPI SILYIDSGNNVYKQYEDMVVESCGR 413

RESULT 5
Q96SBI PRELIMINARY; PRT; 501 AA.
AC Q96SBI;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE DU47704.7 (GROWTH DIFFERENTIATION FACTOR 5 (CARTILAGE-DERIVED
DE MORPHOGENETIC PROTEIN-1)).
GN GDF5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Brown A.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL121586; CAB89416.1;
SQ SEQUENCE 501 AA; 55410 MW; 37985F2D15C4F5EF CRC64;

Query Match 43.9%; Score 771; DB 4; Length 501;
Best Local Similarity 51.1%; Pred. No. 3.7e-59;
Matches 166; Conservative 46; Mismatches 61; Indels 52; Gaps 12;

Qy 9 LRQKYLFDVSMISDKELVGAEELRFRQAPS-----APWGPAGPLHVQLFPCLS--- 59
Db 217 VRKQYVFDISAL-EXDGLLGAEELRLRKPKSTAKPAAPGGGAAQL--KLSSCPSGRQ 273
Qy 60 -PLLLDARTLDPOGAPAGVEFDVQGRH-QPWKQLCLELRAANGELDAGEAEARAG 117
Db 274 PASLLDVRVS--PGLDGSWEVFDIWKLFNFKNSAQLCLELE-AW---ERGRA----- 321
Qy 118 PQQPPPLDLRSLGFRVRPPQERALLVFTSRQK-NL-FAEMRQOLGSAEAGPAGAE 176
Db 322 -----VDRLGCLGFDRAARQVHEKALFLVFGRTKKRDLFENEIKARSGQDDKT----- 368
Qy 177 GSWPPSPGAPDARPLWPSGRRRRRTAFASRHGKGRKSRRLRCSKKPLHVNFKELGWD 236
Db 369 -----VVEYLFQ--RRKRAPLATRQGRPSKNLKRCSRKALHVNFKDMGWD 416
Qy 237 WIITAPLEYAYHCEGVCDPFLRSHLEPTNHAIQTLMNSMDPGSTPPSCCVPTKLPISI 296
Db 417 WIITAPLEYAYHCEGLCEPFLRSHLEPTNHAIQTLMNSMDPESTPTCCVPTRUSPISI 476
Qy 297 LYIDAGNNVYKQYEDMVVESCGR 321
Db 477 LFIDSANNVYKQYEDMVVESCGR 501

RESULT 6
Q9W6G0 PRELIMINARY; PRT; 500 AA.
AC Q9W6G0;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE GDF-5 PROTEIN.
GN Gallus gallus (Chicken).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
```

NCBI_TaxID=9031;
[1]
SEQUENCE FROM N.A.
MEDLINE=99146893; PubMed=10021348;
Francis-West P.H., Abdelattah A., Chen P., Allen C., Parish J.,
Lader R., Allen S., Macpherson S., Luyten F.P., Archer C.W.,
"Mechanisms of GDF-5 action during skeletal development.";
Development 126:1305-1315(1999).
-!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC EMBL: AF123389; AAD30451.1; -
DR HSSP: P12643; 3BMP.
DR InterPro: IPR002405; Inhibin_alpha.
DR InterPro: IPR001839; TGF-beta.
DR Pfam: PF00019; TGF-beta; 1.
DR PRINTS: PR00669; INHIBIN.
DR ProDom: PD000357; TGF-beta; 1.
DR SMART: SM00204; TGF-beta; 1.
DR PROSITE: PS00250; TGF-BETA; 1.
DR Glycoprotein.
SEQUENCE 500 AA; 55952 MW; 1DE8385A3119A598 CRC64;

Query Match 43.0%; Score 756; DB 13; Length 500;
Best Local Similarity 49.5%; Pred. No. 7.4e-58;
Matches 159; Conservative 47; Mismatches 69; Indels 46; Gaps 10;

QY 9 LRROKLYFDVSMDSKEELVCAELRLFRQAPSAPWGPAG--PLHVQLFPC----LSPLL 62
Db IRKQKIPDISAL- EKDLGLVLAELRLKRPSPDTWKSHSGKTSQVKLFSCSTNRQAATL 276
QY 63 LDARTLPOGAPAGVDFVWQGLRH-QPWKOLCLELRAWGEDLAGEAEARAGPQP 121
Db LDRSTVSTDPK--WEVDFIWLFRNFKNLVNLCFELET----FDRGRA----- 320
QY 122 PPDLSRSGFGRVRRPQERALLVFTSRQKRL-FAEMREQLSGAAPGAGAECSWP 180
Db --VLRVTGFRNTRQVNEKALFLVGRKRDLEFNEIKARSQDDKT----- 367
QY 181 PPSGAPDARPLPSGRRRRRTAFASRHGRKSKRLRCKPLHVNFKELGWDWIIA 240
Db -----VYELFNQ--RRKKRAPLATRQGRKPRKALHVNFKMDGMDWIIA 419
QY 241 PLEYEAYHCEGVCDPLRSHLEPTNHAIIQTLMNSMDPGSTPPSCCVPTKLTPTSILYID 300
Db PLEYEAYHCEGLCEFLRSHLEPTNHAIIQTLMNSMDPESTPTCCVPTRLSPISILFID 479
QY 301 AGNNVYKQYEDMVVESCGR 321
Db SANNVYKQYEDMVVESCGR 500

RESULT 7
QYBDW9 ID QYBDW9 PRELIMINARY; PRT; 294 AA.
AC QYBDW9
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE GROWTH/DIFFERENTIATION FACTOR 7 (FRAGMENT).
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=CEREBRAL CORTEX MOTOR AREA;
RX MEDLINE=21136583; PubMed=11238730;
RA Watabe A., Fujita H., Hayashi M., Yamamori T.,
RT "Growth/differentiation factor 7 is preferentially expressed in the
primary motor area of the monkey neocortex.";

J. Neurochem. 76:1455-1464(2001).
-!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC EMBL: AF254567; AAK27794.1; -
DR HSSP: P12643; 3BMP.
DR InterPro: IPR001839; TGF-beta.
DR Pfam: PF00019; TGF-beta; 1.
DR ProDom: PD000357; TGF-beta; 1.
DR SMART: SM00204; TGF-beta; 1.
DR PROSITE: PS00250; TGF-BETA; 1.
DR Glycoprotein.
NON_TER 1
FT NON_TER 1
SQ SEQUENCE 294 AA; 31792 MW; 49B7BCD9F27AF39F CRC64;

Query Match 41.9%; Score 737; DB 6; Length 294;
Best Local Similarity 52.2%; Pred. No. 1.8e-56;
Matches 166; Conservative 28; Mismatches 74; Indels 50; Gaps 10;

QY 30 AELRLFRQAPSAPW-GPPAGPLHVQLFPC----LSPLLDAARTLPOGAPAGWVDFVW 84
Db AELRLFRQAPSAPW-GPPAGPLHVQLFPC----LSPLLDAARTLPOGAPAGWVDFVW 84
QY 85 QGLRH-----QPWKOLCLELRAWGEDLAGEAEARAGPQPDPDLRLSLGF---GRRVR 136
Db QGLRH-----QPWKOLCLELRAWGEDLAGEAEARAGPQPDPDLRLSLGF---GRRVR 136
QY 59 DAMRRHRREPFRPRAFCLLLRVAVTGPVRS-----PLALRLRGFGWPGGGS 104
Db DAMRRHRREPFRPRAFCLLLRVAVTGPVRS-----PLALRLRGFGWPGGGS 104
QY 137 PQRERALLVFTSRQK-NLFAEMREQ---LGSAAAGPGAGAECSWPPSPGADARPLW 192
Db PQRERALLVFTSRQK-NLFAEMREQ---LGSAAAGPGAGAECSWPPSPGADARPLW 192
QY 105 APERALLVSSRTORKEKSLFREMRAQALGAALAAQD-----PDPGTGTGSPRA 156
Db APERALLVSSRTORKEKSLFREMRAQALGAALAAQD-----PDPGTGTGSPRA 156
QY 193 PSGRRRRTAFASRH-----GKRHGKSKRLRCKSKPLHVNFKELGWDWIIAPLE 243
Db PSGRRRRTAFASRH-----GKRHGKSKRLRCKSKPLHVNFKELGWDWIIAPLE 243
QY 244 YEAYHCEGVCDPLRSHLEPTNHAIIQTLMNSMDPGSTPPSCCVPTKLTPTSILYIDAGN 303
Db YEAYHCEGVCDPLRSHLEPTNHAIIQTLMNSMDPGSTPPSCCVPTKLTPTSILYIDAGN 303
QY 217 YEAYHCEGVCDPLRSHLEPTNHAIIQTLMNSMDPAAPASCCVPARLSIPISILYIDAAN 276
Db YEAYHCEGVCDPLRSHLEPTNHAIIQTLMNSMDPAAPASCCVPARLSIPISILYIDAAN 276
QY 304 NVVYKQYEDMVVESCGR 321
Db NVVYKQYEDMVVESCGR 294

RESULT 8
QYBDW9 ID QYBDW9 PRELIMINARY; PRT; 324 AA.
AC QYBDW9
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE GROWTH DIFFERENTIATION FACTOR 5 (FRAGMENT).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LEG BUD;
RX MEDLINE=99119368; PubMed=9918693;
RA Merino R., Macias D., Ganay Y., Economides A.N., Wang X., Wu Q.,
RA Stahl N., Sampath K.T., Varona P., Hurle J.M.,
RT "Expression and function of Gdf-5 during digit skeletogenesis in the
embryonic chick leg bud.";
RL Dev. Biol. 206:33-45(1999).
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL: AF075441; AAD14568.1; -
DR HSSP: P12643; 3BMP.
DR InterPro: IPR002405; Inhibin_alpha.
DR InterPro: IPR001839; TGF-beta.
DR InterPro: IPR001111; TGF-beta.
DR Pfam: PF00019; TGF-beta; 1.
DR Pfam: PF00688; TGF-beta; 1.

```

DR      SMART: SM00204; TGFB: 1.
DR      PROSITE: PS00250; TGF_BETA; 1.
DR      Glycoprotein. 1
FT      NON_TER 1
SQ      SEQUENCE 261 AA; 77346E977036A104 CRC64;

Query Match
39.8%; Score 698.5; DB 13; Length 261;

```

60	PLLLDART---	LDPOGAPPAGWEVDFVWQGLRHQPWKQ-----	LCLELRAANGELD	107
5	PLLLSRTIDLLD	LDTSSATWDFVGPPIK-TPLQKHRTAEDTRLCLLSISA-----	57	
108	AGEAEARARGQQPP	PDLSLGSFGRRVRPPQERALLVFTRSORK-NLFAEMREQLGSA	166	
58	VSDSNNAEVHPGM-----	LGLSREDQOOTHREALLVAFSARKKENLFREIREKIRAM	109	
167	PAECGACAFCSWDD	SCADNABDWI.DSCGRRRRRTAFASB-----	HGKHGHKKSRIR	219

110	KS-----RKFSNPPTPEHSIKGHP-----RAKRRKRRKTLAKRCPCVGPFTISGGAGGGRKRR	139
220	CSKKPLPHVNFKELGWDWIIAPLEYEAYHCEGVCDFPLRSHLEPTNHAIQIOTLMSMDPG	279
160	CSRKPLPHVNFKELGWDWIIAPLEYEAYHCEGLCDFPLRSHLEPTNHAIQIOTLMSMDPE	219
280	STPPSCCVPTKLTPTISILYIDAGNNVYVKQYEDMWVYESCGCR	321
220	STPPSCCVPSKLPISILYIDSGNNVYVKQYEDMWVYESCGCR	261

RESOUR	10	
	042303	
ID	042303	PRELIMINARY; PRT; 257 AA.
AC	042303;	
DT	01-JAN-1998	(TREMBlrel. 05, Created)

DE
GN
OC
OS
OC
OC
OC
OC
OC
RN
RP

CONTACT (FRAGMENT).
GDF5
Zebrafish (Danio rerio)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
NCBI_TaxID=7955;
[1]
SEQUENCE FROM N.A. 0255352.

"Expression of contact, a new zebrafish DVR member, marks mesenchymal cell lineages in the developing pectoral fins and head and is regulated by retinoic acid.";
RL Mech. Dev. 65:163-173(1997).
-!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
EMBL: Y12005; CAA72733.1; -.
HSP: p12643; 3BMP.
ZFIN: ZDB-GENE-990415-39; gdf5.
InterPro: IPR002400; GF_cysknot.
InterPro: IPR001839; TGF-beta.

DR	PRINTS:	PR000438;	GFCYSKNOI.
DR	ProDom:	PD000357;	TGF_beta; 1.
DR	SMART:	SM00204;	TGFB; 1.
DR	PROSITE:	PS00250;	TGF_BETA; 1.
DR	Glycoprotein:	KW	
FT	NON_TER	1	
FT	CHAIN	140	257
SQ	POTENTIAL:		
	SEQUENCE	257 AA;	29787 MW; 6D64F0542F948849 CRC64;
	Query Match	37.8%;	Score 664.5; DB 13; Length 257;
	Best local similarity	51.8%;	Prod No. 33e-50.

Matches 144; Conservative 32; Mismatches 53; Indels 49; Gaps 9;

QY 52 VQLPPCLSL---PLLDARTLDPOGAPPAGWEVFDVW---QGLRHQPWKQLCLELRAANG 104
Db 21 LRLFTCASGKNAVLLQARPDFSHSA--SYWEVFDIWKVKFNRP--QLCLELDA--- 73
QY 105 ELDAEAEARAGPOPPPPDLRLSLGFRVRPPQERALLVVFTRSORKNLF-AEMREOL 163
Db 74 -VDHGR-----PUDLLGLSRAGROTKEKAFVVFVGRTKKRLGFLYNETKAR- 119
QY 164 GSAPAGAGAGAGSPPSPGADPAPWLPSPGRRRRRTAFASRHKGRKSLRSCSK 223
Db 120 -----SGHDKNTVYELVTFQRRMRAPLR-GKKPIKPKQKCNK 159
QY 224 PLHVNKELGWDWIIAPLEYEYHCEGVCDFPLRSHLEPTNHAIIQTLNMSMDPGSTPP 283
Db 160 QLHVNFKEMGWDDWIIAPLEYEAFHCDGVGCDFFIRSHLEPTNHAIIQTLNMSMDPRSTPP 219
QY 284 SCCVPTKLTPIISILYIDAGNNVYKQYEDMVVESCGR 321
Db 220 TCCVPTRLSPISILYIDSANNVYKQYEDMVVESCGR 257

RESULT 11
Q99MY1
ID AC Q99MY1 PRELIMINARY; PRT; 441 AA.
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE GROWTH/DIFFERENTIATION FACTOR 7 (FRAGMENT).
GN GDF7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TT2;
RX MEDLINE=21136583; PubMed=11238730;
RA Wataabe A., Fujita H., Hayashi M., Yamamori T.;
RT "Growth/differentiation factor 7 is preferentially expressed in the
RL primary motor area of the monkey neocortex."
RL J. Neurochem. 76:1455-1464(2001).
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL; AF254571; AAK30843.1; -.
DR EMBL; AF254570; AAK30843.1; JOINED.
DR HSSP; P12643; 3BMP.
DR InterPro; IPR002405; Inhibin.alpha.
DR InterPro; IPR001839; TGF-beta.
DR InterPro; IPR001111; TGFb_N.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR PRINTS; PR00669; INHIBINA.
DR ProDom; PD000357; TGF-beta; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF-BETA; 1.
DR Glycoprotein.
FT NON_TER 441 441
SQ SEQUENCE 441 AA; 45617 MW; 74DA312A853701F0 CRC64;

Query Match 36.1%; Score 634; DB 11; Length 441;
Best Local Similarity 44.5%; Pred. No. 2.8e-47;
Matches 153; Conservative 33; Mismatches 70; Indels 88; Gaps 13;
QY 12 QKLYFDVMSLSDKELVGAELRFOAPSAP-----WGPPAGPLHVQLFP 56
Db 132 QSFLEWSSLEADEVNAELVRLRRSPEDRDSATLLPRLLLSTCPDEAGTAH----- 186
QY 57 CUSPLLDARTLDPOGAPPAGWEVFDVWQGLR-HQPW-----KQLCLELRAWGLDAGEA 111
Db 187 -----LLHSRAAEPLGG--ARWEAFDVTDAVQSHRRPRASRKFCLVLR-----VTASES 235

QY 112 EARARGPOPPPPDLRLSLGFG-----RRVRPPOERALLVVFTRSORKNLF-AEMREOLG 164
Db 236 S-----PLAIRRLGFGWPGCGGGGTAAERALLVVISSRTQKAEESLPREIRAQAR 285
QY 165 SABAAGPAGAGSPPSPGADPAPWLPSPGRRRRRTAFASRHKGRKSLRSCSK 208
Db 286 ALRAA-----AE---PPDPGPGAGSRKANLGGRRRRRTALAGTRGADGSGGGGGGGGG 337
QY 209 -----GKRHGKSLRSCSKPLHVNFKELGWDWIIAPLEYEYHCEGVCDFPL 257
Db 338 GGGGGGGGGAGRGRGRSRKSLHVDYDFKELGWDWIIAPLDYEYHCEGVCDFPL 397
QY 258 RSHLEPTNHAIIQTLNMSMDPGSTPPSCCVPTKLTPIISILYIDA 301
Db 398 RSHLEPTNHAIIQTLNMSMDPADAAPASCVCVPARLSPISILYIDA 441

RESULT 12
O93573
ID AC O93573 PRELIMINARY; PRT; 126 AA.
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE PUTATIVE GROWTH/DIFFERENTIATION FACTOR 6/7 (FRAGMENT).
GN GDF6/7.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99026113; PubMed=9808626;
RA Lee K.J., Mendelsohn M., Jessell T.M.;
RT "Neuronal patterning by BMPs: a requirement for GDF7 in the generation
RT of a discrete class of commissural interneurons in the mouse spinal
RL cord";
RL Genes Dev. 12:3394-3407(1998).
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL; AF089086; AAC97113.1; -.
DR HSSP; P12643; 3BMP.
DR InterPro; IPR002400; GF_cysknot.
DR InterPro; IPR002405; Inhibin.alpha.
DR InterPro; IPR001839; TGF-beta.
DR Pfam; PF00019; TGF-beta; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PRINTS; PR00669; INHIBINA.
DR ProDom; PD000357; TGF-beta; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF-BETA; 1.
DR Glycoprotein.
FT NON_TER 1 1
SQ SEQUENCE 126 AA; 14265 MW; CB824D280F44A394 CRC64;

Query Match 34.9%; Score 612.5; DB 13; Length 126;
Best Local Similarity 86.5%; Pred. No. 4.9e-46;
Matches 109; Conservative 10; Mismatches 6; Indels 1; Gaps 1;
QY 197 RRRRTAFASRHKGR-HGKRSRLRSCSKPLHVNFKELGWDWIIAPLEYEYHCEGVCDF 255
Db 1 RRRRTTAAARSGRGGHKKAKTRCSRKPLHVNFKELGWDWIIAPLDYEYHCEGVCDF 60
QY 256 PLRSHLEPTNHAIIQTLNMSMDPGSTPPSCCVPTKLTPIISILYIDAGNNVYKQYEDMV 315
Db 61 PLRSHLEPTNHAIIQTLNMSMDPESTPPSCCVPSKLSILYIDSGNENVYKQYEDMV 120
QY 316 ESCGCR 321
Db 121 ETGCR 126

```

RESULT 13
Q90Y82 ID Q90Y82 PRELIMINARY; PRT; 277 AA.
AC Q90Y82;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE LJBM2/4A (FRAGMENT).
GN LJBM2/4A.
OS Lampetra japonica (Japanese lamprey) (Entosphenus japonicus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hypercoartia;
OC Petromyzontiformes; Petromyzontidae; Lethenteron.
OX NCBI_TaxID=94989;
RN [1]
RP SEQUENCE FROM N.A.
RA Shigetani Y., Sugahara F., Kawakami Y., Murakami Y., Hirano S.,
RA Kuratani S.;
RT "Shape precedes structure: an exaptation for the vertebrate jaw
evolution.";
Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
EMBL; AB071890; BAB6395.1; -.
FT NON_TER 1
SQ SEQUENCE 277 AA; 30507 MW; 30FB94C547AD99B0 CRC64;

Query Match 25.7%; Score 451; DB 13; Length 277;
Best Local Similarity 34.5%; Pred. No. 1.5e-31;
Matches 112; Conservative 45; Mismatches 98; Indels 70; Gaps 13;

QY 19 SMLSKEELVGAELRLFRQAPSAPGPPAGPLH-VQLFPLSPILLD-----ARTLDPQ-- 71
Db 1 SSIPGGEVTSALHVIYERLS---GPARAALHRIINVYEVLRPAADGTPARLLDTRV 57
QY 72 GAPPAGWEFV-----WQGLRHQPKQLCLCELAAGELDGAEEARARGPQPPPPD 125
Db 58 HSGRSEMERFVSPAAVRAAAR-APNHGLLVEVH-----HLDGGTPEKR----- 101
QY 126 LNSLGRVRPPOERALLVTRSORKNLFAEMREQLGSAEAGAGAGAGSWPPPSGA 185
Db 102 -RHVRIGRSLH-----AEAVAAARDGAGEGGDG-----EGW 133
QY 186 PDARPWLPs---PGRRRRTAFASRGRH-----GKSLRCLSKPLHVNFKELGWD 236
Db 134 POLRPLVTFGHDGKTRDGTLLRPPKRSRPNKGRGRCQARYFLYVDFSDVGWND 193
QY 237 WIAPLEYEAYHCEGYCDPPLRSHLEPTNHAIQTILMSMDGPPSCCVPTKLTPISI 296
Db 194 WIVAPPGYNAPFCQGCHEFLPQHLNSTNHAIQVTLVNSVNP-EVPRACCIPTLTPIAL 252
QY 297 LYIDAGNNVYKQYEDMNVESGCR 321
Db 253 LYIDAEKVKVLYKQYEDMNVESGCR 277

RESULT 14
Q9XYQ7 ID Q9XYQ7 PRELIMINARY; PRT; 417 AA.
AC Q9XYQ7;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE BONE MORPHOGENETIC PROTEIN BMP2/4.
GN BMP2/4.
OS Lytechinus variegatus (Sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Echinacea; Echinoidea; Strongylocentrotidae;
OC Lytechinus.
OX NCBI_TaxID=7654;
RN [1]
RP SEQUENCE FROM N.A.
RA Angerer L.M., Oleksyn D.W., Logan C.Y., McClay D.R., Dale L.,
RA Angerer R.C.;

```

```

RT "A BMP pathway regulates cell fate allocation along the sea urchin
animal-vegetal embryonic axis.";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL; AF119712; AAD28038.1; -.
DR HSSP; P12643; 3BMP.
DR InterPro; IPR002405; Inhibin_alpha.
DR InterPro; IPR001839; TGF-beta.
DR InterPro; IPR001111; TGF-beta.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGF-beta; 1.
DR PRINTS; PR00669; INHIBIN.
DR ProDom; PD000357; TGF-beta; 1.
DR SMART; SM00204; TGF-beta; 1.
DR PROSITE; PS00250; TGF-BETA; 1.
KW Glycoprotein.
SQ SEQUENCE 417 AA; 47727 MW; 5EB93E3022BFC50F CRC64;

Query Match 24.3%; Score 427.5; DB 5; Length 417;
Best Local Similarity 31.5%; Pred. No. 2.7e-29;
Matches 108; Conservative 54; Mismatches 100; Indels 81; Gaps 11;

QY 7 TPLRRQKYLFDVSMLSKDEELVGAELRLFR-----QAPSAPWGPAGPLH---VQ 53
Db 128 TEHRHTVIFNISTMPAEVEVLTMAELRFRKDLLEHSHIAKRHALDDRKSLPIHYMORIN 187
QY 54 LFPCLSPV-----LLDARTLDPOCAPGAGWEFV-----WQGLRHQPKQLCLE 98
Db 188 VFHILKPVARNRDTIKRLDRLVDVRN---SSNESDVRPAVTSWEV---PEKNHGLE 241
QY 99 LRAANGELDGAEEARARGPQPPPPDLRLSGFGRVRRPPOERALLVTRSORKNLFAE 158
Db 242 I-----EL-----IDSRGR-----PSPNHHVVRVTRADPSKVQEL-----QNEEDERWFQ 282
QY 159 MREOLGSAEAGAGAGAGSWPPPSGADPARPWLPSGRRRRRTAFASRGRHKGKSR 218
Db 283 TRQILVYSDDG-----RTKSPSRGRKRKRKRLKA 314
QY 219 RCKSKPLHVNFKELGWDWIAPLEYEAYHCEGYCDPPLRSHLEPTNHAIQTILMSMDP 278
Db 315 NCRHRLPVDFSDVHNDWIVAPAGYQAYCHGCEPFLAEHLNTHAIQVTLVNSVNP 374
QY 279 GSTPSCCVPTKLTPIISLYIDAGNNVYKQYEDMNVESGCR 321
Db 375 ALVPKACGCGPTLSAISMLYLDYEYKVKVLYKQYEDMNVESGCR 417

RESULT 15
Q9XYQ8 ID Q9XYQ8 PRELIMINARY; PRT; 289 AA.
AC Q9XYQ8;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE BONE MORPHOGENETIC PROTEIN BMP2/4 (FRAGMENT).
GN BMP2/4.
OS Strongylocentrotus purpuratus (Purple sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Echinacea; Echinoidea; Strongylocentrotidae;
OC Strongylocentrotus.
OX NCBI_TaxID=7668;
RN [1]
RP SEQUENCE FROM N.A.
RA Angerer L.M., Oleksyn D.W., Logan C.Y., McClay D.R., Dale L.,
RA Angerer R.C.;
RT "A BMP pathway regulates cell fate allocation along the sea urchin
animal-vegetal embryonic axis.";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL; AF119713; AAD28039.1; -.
DR HSSP; P12643; 3BMP.
DR InterPro; IPR002400; GF_cysknot.

```

```

DR InterPro: IPR002405; Inhibin_alpha.
DR InterPro: IPR001839; TGF-beta.
DR Pfam: PF00019; TGF-beta; 1.
DR PRINTS: PR00438; GFCYSKNOT.
DR PRINTS: PR00669; INHIBINA.
DR ProDom: PD000357; TGF-beta; 1.
DR SMART: SM00204; TGF-beta; 1.
DR PROSITE: PS00250; TGF-BETA; 1.
KW Glycoprotein.
FT NON_TER 289
FT NON_TER 289
SQ SEQUENCE 289 AA; 33599 MW; 99E175C7DBC3C58B CRC64;

Query Match 24.2%; Score 426; DB 5; Length 289;
Best Local Similarity 31.7%; Pred. No. 2.4e-29;
Matches 106; Conservative 54; Mismatches 96; Indels 78; Gaps 11;

QY 16 FDVSMLSKDELVGAEURLRFR-----QAPSAPGWGPAGPLH-----VQLFFCLSP- 61
.. 2 FTVSTMPEEEVMTAEURLRFLKDLDEHHIVKRRHALHDRESLKPITYHQRIINVYHILKPV 61

JY 62 -----LLDARTLDPOGAPPAGWVEFDVWQGLR---HQPWKOLCLLELRAAWGELDAGE 110
DB 62 RNRDTIKRLIDTRLVDVNR---ASWESFDVPRAMVWLEEPKHNGLLEI-----EL---- 109

QY 111 AEARARCPQPPPDRLSLGFGRRVRPQGRALLVVTFRSQRKNLFAEMREQLGSAAG 170
DB 110 IDSRGR-----PSPNHHHVTRTREADPSKVEEL-----ENEEDRWFTQRPQIVTSDGG 159

QY 171 PGAGAEGSWPPSPGAPDARPWLPSGGRRRRTAFASRHG---KRCHKKSLRCSKKPLH 226
DB 160 -----RTRKSPSSSSSGRGQKKRKKGLKANCRRRHELY 192

QY 227 VNFKELGWDDWIIAPLEYEAYHCEGVGDFPLRLSHLEPTNHAIITQLMNSMDPGSTPPSCC 286
DB 193 VDFSDVHNDWIAPAGYQAYCRGECFPFLAEHLNTNHAIVQTLVNSVPALPVKACC 252

QY 287 VPTKLTPIISILYDAGNNVYKQYEDMWVESCGC 320
DB 253 VPTELSAISMLYLDEYEKVYLLKNYQDMVVEGCGC 286

```

Search completed: October 3, 2002, 15:45:37
Job time: 413 sec